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March 25, 2005, 00:03:32 ; Search time 9715 Seconds
   (without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AX146795 Sequence	S83325 aspartvl (as	CO871564 Sequence	U03109 Human aspar	M91213 Bos taurus	AF289486 Mus muscu	AF289487 Mus muscu	CO729666 Seguence	AF289489 Homo sapi		BD234762 Gene enco			AR441744 Seguence		AX369081 Seguence		BC025236 Homo sapi	AF289488 Mus muscu
SUMMARIES	ID	AX146795	583325	CQ871564	HSU03109	BOVASBHY	AF289486	AF289487	CQ729666	AF289489	BC015518	BD234762	AR274038	AR277619	AR441744	AR532049	AX369081	AF306765	BC025236	AF289488
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æ	Query	100.0	100.0	99.9	98.8	63.7	62.4	62.4	52.3	40.7	35.7	35.2	35.2	35.2	35.2	35.2	35.2	33.5	29.5	19.6
	Score	2324	2324	2320.8	2296.8	1480.4	1450.2	1450.2	1215.8	947	829.6	819	819	819	819	819	819	779.4	619	455.8
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	241 TIGITGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGAG 300 	ATTTGATGTGGATGCCAAAGTTTTATTAGGACTTAAAGAGAGAG	CIACITCAGAGC 38 AGGITCCIGIGG 42		421 AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG 480 	ANATEGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAG 54	AAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGTACCACCACAG 54 GAGAACCACAAAAGAGGGTGATGATTTCTTATGGCGACTGATGTAGATGATAGATTTG 60	541 GAGAACCACAACAAGAGGATGATGATTCTTATGGCGACTGATGTAGATGATAGATTTG 600 601 AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCCATAGTTACCACGTGGAAGAGA 660		661 CAGTITCACAAGACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAATCCAG 720 	ATTCCAGTGAACC	84	GAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCA 8	841 CAGAAGTAACTGCTCCCCCGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG 900 	AAGTAAGCATTTTTCCT	, 4	CAGATGATCCAGAACAAAAGCAAAAGTTAAGAAAAAGAAGCCTAAACTTTTAAATAAA	1021 TTGATAAGACTATTAAAGCTGAACTTGATGCTGCAGAAAAACTCCGTAAAAGGGGAAAAA 1080 		CATTTAAAGAACTAGTACGCAAATAACCCT CAGAGT CCACGAG AGTGTGAGGATGATTTGGCTGAGAAGAGGAGAAGTAATGAGG	3 120	1201 TGCTACGTGGAGCCATCGAGACCTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGCAG 1260 1201 TGCTACGTGGAGCCATCGAGACCTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGCAG 1260		
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AKVLLGLERRSTSERPAPPEREREWYPERPERPROWNERTELPEPSSHETTBERSTYPDET
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SQDCNQDMEEMMSEQENPDSSERVVEDERLHIDTDDVTYQVYEEQAVYEPLENTY
SQDCNQDMEEMMSEQENPDSSERVVEDERLHIDTDDVTYQVYECQAVYEPLENTY
SNEVTIKAALEDAAEKLAKSTERAVANSTELAKTROPREGATICAGNAY
RSNEVLRGAIETVQGVSLLGDNDDAKKYYEETLSKREDRQGFGHNGGSLLTLQBLACK
RSNEVLRGAIETVQGVSLLGDNDDAKKYYEETLSKREDRQGFGHNGGSLLTLQBLACK
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TNORLRWHHGLIGUY IPROGCKIRRANETTWEEGKVLIFDDSFEHEWWQDASSFRLIFIV
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                                                                                   Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammallai, Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2324)
Lavaissiere, L. Jia, S., Nishiyama, M., de la Monte, S., Stern, A.M., Wands, J.R. and Friedman, P.A.

Voverexpression of human aspartyl (asparaginyl) beta-hydroxylase in hepatocellular carcinoma and cholangiocarcinoma
J. Clin. Invest. 98 (6), 1313-1323 (1996)
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                                                                                                                                                                                                                                        GenBank staff at the National Library of Medicine created this entry (NCBI gibbsq 179962) from the original journal article. Authors note differences between this sequence and that of F. Korioth. C. Gieffers, and J. Frey: Gene 150 (2), 395-399 (1994), GenBank U03109.
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    2324
    7gene="aspartyl" (asparaginyl) beta-hydroxylase, HAAH"
    2288
    7gene="aspartyl" (asparaginyl) beta-hydroxylase, HAAH"
    note="HAAH"

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100.0%; Pred. No. 0;
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/mol_type="maxAA"
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1. 2324
2324
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HepG2, mRNA Partial,
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S83325.1 GI:1911651
                                                         Homo sapiens (human)
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                         ATGAAGAGGTGCTGAGTGTGCCTAATGATGCCTTTGCTAAAGTCCATTATGGCTTCA
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                                         Murphy,F.J., Sheehan,D.E., Keating,K.E., Hayes,I.E. and Enzymes involved in apoptosis
Enzymes involved in apoptosis
Patent: WO 2004078783.4 55 16-SEP-2004;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Primates;
Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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CQ871564 Sequence 55 from Patent CQ871564 CQ871564.1 GI:52745624

RESULT 3
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AKVLLGLKERSTSEPAVPPEBAEPHTEPEEQVPVBAEPQNIEDEAKEGIQSLLHEMVH
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TEVTAPPEDNPVEDSQVIVEEVSIFPVEBQLSKRYPVERGAVTEPLERKKKPTLI
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VHEE YDEGO YDEGO KTIKE KTIKE ALKAU BGIEE KAQPE TLWQ LIRMHI ORIGIN Best Local Similarity	Matches 1903; Conservat Qy 1 CGGACCGTGCAA Db 178 CGGTGCGCGCG Qy 58 GCGGCTCGGGA	238 112 298 172	Db 358 TTTTCATCATICTT Qy 232 GGTTTGATCTTG Db 418 GGTTTGATCTTG Qy 259 Db 478 TGTCAGAGGTAC Qy 307 ATGTCGATGATG Db 538 ATGTCGATGATG Db 538 ATGTCGATGATG	Oy 367 TCCCGCCAGAAG Db 598 TGCCACCAGAAG OY 427 AACCCAGAATA Db 658 GACGTCAGAATA OY 487 TACACGCAGAATA	Db 715 TATACTCAGAAC Qy 547 CACAACAGAG Db 769 ACTGCAGCCCG Oy 607 TGGAACTGCAGG Db 829 TGGGAACTGCAGG	Oy 667 CACAAGACTGTAA Db 889 CGCCGAGCCTACAA Oy 727 GTGAACCAGTAG Db 949 GTGAACCAGTAG Oy 781 ACCAAGTCTATG
1924 AAAACCTGAGGAAAAAGGGGACTGGAGCCAGTTCACGCTGTGGCAGCAAGGAAGAAGAA 1921 ATGAAAATGCCTGCAAAGGAGCTCCTAAAACCTGTACCTTACTAGAAAAGTTCCCCGAGA 1984 ATGAAAATGCCTGCAAAGGAGCTCCTAAAACCTGTACCTTACTAGAAAGTTCCCCGAGA 1981 CAACAGGATGCAAAGGAGACTCCTAAATATTCCATCATACTAGAAAGTTCCCCGAGA 1981 CAACAGGATGCAAAGAGAACAAAATATTCCATCATCATACTAGAACTCCCGAGACTCCCGAGA 2041 CAACAGGATGCAAAAGAGAACAGAACAAAATTCCATCATGCACCCCGGGACTCACGTGT 2041 GGCCGCACACAGGACCCAAAACTGCAGGCTCCCAAATGCACCTGGGCTTGGTGTCCCAAAGATCCACAAACTGCAGGCTCCCAAATGCACCTGGGCTTGGTGTTCCCAAAACTGCACCCCGAAATGCACCTGGGCTTGGTGATTCCCAAAACTGCAGGCTCCCAAATGCACCTGGGGCTTGGTGATTCCCAAACTGCAGGCTCCCAAATGCACCTGGGGCTTGGTGATTCCCAAACTGCAAACTGCAGGTCCCGAATGCACCTGGGGCTTGGTGATTCCCAAACTGCAAACTGCAGGCTCCCAAATGCACCTGGGGCTTGGTGATTCCCAAACTGCCAAAACTGCAGGCTCCCAAATGCACCTGGGGCTTGGTGATTCCCAAACTGCCAAAACTGCCCCCAAAACTGCCCCAAATGCACCTGGGGCTTCGTGATTCCCCAAACTGCCCCAAAACTGCCCCCCAAAACTGCCCCCCCC		Oy 2221 TATTCATCGTGGGTGTGGCATCCGGAACTGACCCACAGAGGCGTGCCGG 2280 Db 2284 TATTCATCGTGGATTGTGGCATCCGGAACTGACACCACAGAGAGACGAGCCTTCCAG 2343 Oy 2281 CAATTTAGCATGAATTCATGCAAACTTGGGAAACTCTGGAAGA 2324 Db 2344 CAATTTAGCATGAATTCATGCAAGCTTGGGAAACTCTGGAAGA 2387	RESULT 5 BOVASBHY LOCUS BOVASBHY LOCUS BOYASBHY ACCESSION BOYASBHY ACCESSION B1213 BOYASBHY ACCESSION B1213 BOYASBHY ACCESSION B1213 BOS taurus (cow) BOS T	Editation (2013) RS Jia,S., VanDusen,W.J., Diehl, R. Elilaton,K.O., Stern,A.M. and CDNA cloning and expression of Deta-hydroxylase AL J. Biol. Chem. 267 (20), 1432/NB 92332546 ED 1378441 RS Friedman,P.A.	Direct Submission Submitted (15-APR-1992) P.A. Frie Research Laboratories, West Point Original source text: Bos taurus Location/Qualifiers 1. 2739 Acres Host Laurus And type="mRNA"	CDS //LISUNE_TOPE="IIVET and Drain" 1892453

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ATHGIN IPREGCKIRCANETRTWEEGKVLIFDDSFEHEVWQDAASFRLIFIVUDWH
ATHORNSLLPAI
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171 237 111 297 357 231 417 258 477 306 537 366 597 426 57 CATGGAGGACACAGAATGGGAGGAGGCGGACTCTCGGGAACTTCAT CTTCAAGGAAAACTTGGAATCTATGATGCTGATGGTGATGGAGATTTTG ATGCCCAGCGTAAGAATGCCAAG---AGCAGCGGCAACAGCAGCAGCA TITATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTT TTCTAGGAAAACTAGGAATCTATGATGCTGATGGAGATTTTG GTTGACTATGAGGAAG GAGGCTGAGCCACACTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAG 63.7%; Score 1480.4; DB 4; Length 2739; 79.8%; Pred. No. 3.2e-310; ative 0; Mismatches 346; Indels 135; Gaps

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4GTCAAGATATGGAAGACATGATGTATGAGCAGGAAAATCCAGATTCCA

GATGATTTTTTTTTTTTTGCGACTGATGTTGATTTTGAGACCC

909 828 999 888 726 948 780 PAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCA 840

STAGAAGA-----TGAAAGATTGCACCATGATACAGATGATACAT

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GAGGCAGACATGTACCTTGGCTGGAAGATCAGGTTCTGGAGAGCCCAG

DD 1921 ATCARACTGAGGGAAAAGGGTGACTGATTTACGCTGTGGCAGCAAGGAAAAA 2085	RESULT 6 AF289486 LOCUS DEFINITION MUS musculus aspartyl beta-hydroxylase 4.5 kb transcript (Asph) mRNA, complete cds; alternatively spliced. ACCESION AF289486.1 GI:11878109 VERYORDS NUS musculus (house mouse) ORGANISM Mus musculus (house mouse) ORGANISM Mus musculus (special craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. AUTHORS Dinchuk, J. E., Henderson, N. L., Burn, T. C., Huber, R., Ho, S. P., Link, J., O'Nell, K. T., Focht, R. J., Scully, M. S., Hollis, J. M.,	TITLE Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with junctin JOURNAL J. Biol. Chem. 275 (50), 39543-39554 (2000) MEDLINE 20564328 PUBMED 1095665 REFERRNCE 2 (Dases I to 4419) AUTHORS Priedman, P.A. TITLE Direct Submission TITLE Direct Submission JOURNAL Submitted (26-JUL-2000) Applied Biotechnology, DuPont Pharmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400, USA	PEATURES
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0; Mismatches 378; Indels 96; (
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Best Local Similarity 79.5%;
Matches 1833; Conservative (
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Matches 1833; Conservative (
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mRNA, complete cds; alternatively spliced.
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Dinchuk, J.E., Henderson, N.L., Burn, T.C., Huber, R., Ho,S.P., Link, J., O'Neil, K.T., Focht, R.J., Scully, M.S., Hollis, J.M., Appartyl beta - hydroxylase (ksph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 2680)
Dinchuk, J.E., Henderson, N.L., Burn, T.C., Huber, R., Ho, S.P.,
Link, J., O'Neil, K.T., Focht, R.J., Scully, M.S., Hollis, J.M.,
Hollis, G.F. and Friedman, P.A.
Aspartyl beta - hydroxylase (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
                                                                                                                                                                                                 1671 TGCAGAAQAGGACAGATCAAATATTCCATCATGCACCCCGGGACTCACGTGTGGCCGCAC
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1551 AGGGAAAAAGGGGACTGGAGCCAGTTCACGCTGTGGCAGCAAGGAAGAAGAATGAAAT
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                                                            AGGGAAAAAGGGGACTGGAGCCAGTTCACGCTGTGGCAGCAAGGAAGAAGAATGAAAAT
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Dinchuk, J.E., Henderson, N.L., Burn, T.C., Hollis, G.F. and
Priedman, P.A.
Direct Submission
Submitted (26-JUL-2000) Applied Biotechnology, DuPont
Pharmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400,
Location/Qualifiers
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/note="Humbug; asparaginyl beta-hydroxylase; AspH;
non-catalytic isoform; alternatively spliced"
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/organism="Homo sapiens"
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                                                                             Length 1970;
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                                                                            Score 1215.8; DB 6; Length
Pred. No. 7.5e-253;
0; Mismatches 141; Indels
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/db_xref="taxon:9606"
                                                                            Similarity 90.2%; 90; Conservative (
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I (Dasea 1 to 1080)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausmar,R.D., Collins,F.S., Wagner,L., Shemmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Mang,J., Haish,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Scheetz,T.E., Brownsteein,M.J., Uddin,T.E., Toshiyuki,S.,
Carninci,P., Prange,C., Raba,S.S., Loquellano,N.A., Peters,G.J.,
Morsernan,R.J., Malahy,S.J., Bosak,S.A., McEwan, P.J.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,B.J., Hulyk,S.W.,
Fahey,J., Helton,E., Ketteman,M., Wadan,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Schmitz,J., Lockson,M.C., Rodrigues,S.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerth,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
Numan and mouse cDNA sequences
Farens, Marra, M. Solder, Sci. U.S.A., 99 (26), 16899-16903 (2002)
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On Aug 25, 2003 this sequence version replaced gi:15930166.
Contact: MGC help desk
Email: cgapbs.r@mail.nih.gov
Issue Procurement: DCTP/DTF/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
ENNA Library Arrayed by: The I.M.A.G.E. Consortium (CLNL)
NA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                           1080 bp mRNA linear PRI 30-SEP-2003
Homo sapiens aspartate beta-hydroxylase, mRNA (cDNA clone
MAGE:3887962), partial cds.
BC015518
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14589859.
Location/Qualifiers
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Strausberg, R.
Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                   841 CAGAAGTAACTGCTCCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG
                                                            901 AAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCACCAGAAACAAATAG 955
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BC015518,2 GI:34189304
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/product="aspartyl beta-hydroxylase 2.8 kb transcript"
/protein id="AAG40811.1"
/db_xref="G1:11878116"
/db_xref="G
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Pred. No. 1.5e-194;
0; Mismatches 5; Indels (
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larity 99.5%;
Conservative (
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Best Local Similarity
Matches 950; Conserv
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                                        CAGITICACAAGACIGIAAICAGGAIAIGGAAGAGAIGAIGICIGAGCAGGAAAAICCAG 720
                                                                                                                                ATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATACAGATGAACAT 780
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1 (bases 1 to 2442)
Radosevich,J.A.
Gene encoding cancer marker labyrinthine
Patent: JP 2002512005-A 1 23-APR-2002;
JAMES A RADOSEVICH
JAMES A RADOSEVICH
C12N15/09,007K14/47,C07K16/18,C12P21/08,C12Q1/02,C12Q1/68//
(C12P21/08,C12R1:91).C12M15/00
Gene encoding cancer marker labyrinthine
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Pred. No. 8.4e-167;
0; Mismatches 10;
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Gene encoding cancer marker labyrinthine.
BD234762
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    .2442
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

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JP 2002512005-A/1
23-APR-2002
11-MAR-1999 US 09/040485
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98.8%;
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Homo sapiens (human)
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Best Local Similarity 98.8
Matches 825; Conservative
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KEYWORDS
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RKGGLSGTSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDD
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                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1887962"
/tissue_type="lung, carcinoma, large cell
undifferentiated."
/clone_lib="NIH_MGC_69"
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Pred. No. 4.2e-169;
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                                                                                                                     'note="Vector: pCMV-SPORT6
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/db_xref="GI:34189305"
                 organism="Homo sapiens"
                                                                                                                                                                                                                               'codon_start=1
'product="ASPH_protein"
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/db_xref="MIM:600582"
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Unclassified.
Unclassified.
1 (bases 1 to 2442)
Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S.,
Carter,D., Retter,M.W., Mannion,J., Fan,L. and Wang,A.
Compositions and methods for the therapy and diagnosis of lung
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/mol_type="genomic DNA"
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           US 6509448-A 1791 21-JAN-2003
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/organism="unknown"
/mol_type="genomic DNA'
                   Location/Qualifiers
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98.8%;
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Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S., Carter, D., Retter, M.W., Mannion, J. and Fan, L. Compositions and methods for the therapy and diagnosis of lu
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RESULT 14 AR441744 LOCUS DEFINITION

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              901 AAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCACCAGAACAAATAG 955
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ALIGNMENTS

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OKIGIN	John
Query Match	Query Match
Best Local Si	Best Local Similarity 96.7%; Pred. No. 0;
Matches 2055;	Matches 2055; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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Pan troglodytes ASPH gene, VIRTUAL TRANSCRIPT, partial sequence, genemic survey sequence. Ax405268
                                                                                                                                                                                                                               Clark.A.G., Glancwski,S., Nielson,R., Thomas,P., Kejariwal,A., Tolark.A.G., Glancwski,S., Nielson,R., Thomas,P., Kejariwal,A., Todan,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Adams,M.D. and Cargill,M. White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. White,T.J., Sninsky,J.J., Direct Submission
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
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E Adachi, J., Ahizawa, K., Akimura, T., Hara, A., Hashizume, W.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, W., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Nakamara, M., Nishi, K., Nomura, K., Numaza, M., Ohnsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Muramatsu, M., and Hayashizaki, Y., Yasunishi, A.,
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RKRGKIEEAVNAFEELVRKYPOSPARAYGRAQCEDDLAEKGSBNEVLERAIETVOBAA
DLPDAPTDLVKLSLKRRSEKQPLGHMRGSLLTLQRLVQLFPSDTTLKNDLGVSYLLL
GDNDSAKKVYEEVLINTPNDGFAKVHYGFILKAQNKISESIPYLKGGIESGDPGTDDG
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TEUVKSLERWWKLIRDEGLWWMDKARGLFLPEDEDRILBEKGBOGPTLMOGGRKORDAC
KGAPKTCALLEKFESTTGCRRGJKYS IMHFCTHVWPHTGPTNCRLERMILGLVYPKEG
CKIRCANETRTWEEGKVLIPDDSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPA
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(MGD|MGI:1914186, GB|NM_023066, evidence: BLASTN, 99%,
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AKHGGHKNGRRGGISGGSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGVYDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Submiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome.res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
| dev_stage="11 days pregnant adult"
                                                                                                                                                     The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                    FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
                          Exploration Research Group Phase II
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URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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/db_xref="taxon:10090"
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/protein_id="BAC26882.1"
/db_xref="G1:26326277"
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/strain="C57BL/6J"
                                                                                                            Nature 409, 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunco, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Ishikawa, T., Ozawa, M., Ohara, E., Watchiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramstsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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1675 ACTITGCATCTGTCTGGCAACGCTCACTCTACAATGTGAATGGACTGAAAGCACAGCCTT 1734
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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435 GTCGATTATGAAGAAGTTCTAGGAAAACTAGGAGTCTATGATGCGGATGGAGGAC 494 303 TTTGATGTGATGATGCCAAAGTTTTATTAGGACTTAAAGAAGAGTCTACTTCAGAGCCA 362	8 8 8 8 8	1380 AAAATGACCTTGGCGTGGGATACCTCTTGATAGGAGATAATGACAATGCAAAGAAAG
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GODDPDVDDAKVLLGLKERS PSERTFPPEEEAETHAELEGAPBGADI QWYDDEVKDD
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GOSLLGBSWITDHDIAEADGLAGEPQPEVEDFLTVYDSDDRFBDLEPGTWHBEI EDYTH
VEDTASQNHPNDMEEMTNEGENS EEVRHQDYDE PVY EPSEHEGVAL SDNT I DDSS I I S
BEINNASVEBCODTPPYKKKKKLLIKFEDKTIKREDIAEKRRKKK EBANNAFBEL
VRKYPGS PRARYGKACEDDLAEKQRS NEULIKRAI ETYQBAADLPDAFTDLWLSLKR
RSERQQFLGHNRGSLITLQRLWQLF PSDTTLKNDLGWGYHLLGDNDSAKKVY EEVLNV
TPNDGPAKKYYGFI LKAQNKI SESI PYLKEGI ESCOPTGDDRSKYYHLLGDNDSAKKVY EEVLNV
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(MGD|MG1:1914186, GB|NM_023066, evidence: BLASTN, 99%,
match=4404)
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/dev stage="7 days embryo"
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TGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETRTWEEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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/db_xref="G1:26340240"
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Location/Qualifiers
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3924 bp mRNA linear HTC 03-APR-2004 Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched library, clone:C430018B11 enriched library, clone:C430018B11 product:aspartate-beta-hydroxylase, full insert sequence.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                  2154 TGGCCGCATACAGGACCCACAAACTGCAGGCTCCGAATGCATCTGGGGTTAGTGATCCCC
                                TGGCCGCACACAGGGCCCACAAACTGCAGGCTCCGAATGCACCTGGGCTTGGTGATTCCC
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High-efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
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/bc.xref="G1:26330882"
/translation="WYTALLGVWTSVAVVWFDLVDYEEVLGKLGVYDADGDGDFDVDD
AKVLLGLKERSPSERTFPPFEREAETHAELEEQAPEGADIQNVEDEVKEQIQSLLGESV
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EQQDTPPVKKKKKRKLINKFDKT I KAELDAAEKLRKRGK I EEAVNAFEELVRKY PQS PR
ARYGKAQCEDDLAEKQRSNEVLRRA I ETYQEAADLPDAPTDLVKLSLKRRSERQQFLG
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YSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKBGCKIRCANBTRTWEEGKVLIFDDSFB
HEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI"
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                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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                      Kanagawa 230-0045, Japan (E-mail:genome-res6gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.3%; Score 1332.6; DB 3; Length 2854; ilarity 78.6%; Pred. No. 0; Conservative 0; Mismatches 339; Indels 132;
                                                                                                                                                                                                                         prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="FANTOM_DB:9530097J16"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="9530097J16"
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/strain="C57BL/63"
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                                                                                                                                                                                          AKU35,735
Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530097J16
product:aspartate-beta-hydroxylase, full insert sequence.
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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6 (bases 1 to 2854)
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1551 GGAATAGAATCCGGGCATCGCAAGAATTTTTTTTTTTTT	AY405269 LOCUS LOCUS LOCUS DEFINITION Mus musculus ASPH gene, VIRTUAL TRANSCRIPT, partial sequence, ACCESSION AY405269 AY406269 AY406ATCH AY40
11	1251 GTCCCTGCAGACCTGCTGAAGCTTGAAGCCTCAGACAGAC

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1829 TAAAGCCAAAGGTCTTCCTGCCTGAGGATGAAAACCTGAGGGAAAAAGGGGACTGGAG 1888
749 AAGATTGCACCATGATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATA
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            Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Lu, F., Murphy, B., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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54.4%; Score 1264; DB 9;
Best Local Similarity 69.5%; Pred. No. 5.6e-313;
Matches 1465; Conservative 0; Mismatches 638;
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/db_xref="taxon:10090"
                                                                                                                                                           <1. .>2153
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BX403636.2 GI:46924400
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                                                                                                121 AAGTTAAGAAAAGAAGCCTAAACTTTTAAATAAATTTGATAAGACTATTAAAGCTGAAC
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                     925 AACAGCAGGAAGTACCACCAGAAACAAATAGAAAAACAGATGATCCAGAACAAAAAGCAA
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1 (bases 1 to 1050)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Ontional Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: capabs-rémail.nih.gov

Tissue Procurement: ATC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.linl.gov

Plate: Libral 2004

Plate: Libral 2004

Plate: Libral 2004

Plate: Libral 2004

Plate: Libral 2004
CCAGTTCACGCTGTGGCAGCAAGGAAGAAATGAAAATGCCTGCAAAGGAGCTCCTAA 1948
                                                                                                       1949 AACCTGTACCTTACTAGAAAAGTTCCCCGAGACAACAGGATGCAGAAGAGAGACAGATCAA 2008
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AGENCOURT_6543030 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548943
5', mRNA sequence.
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequence fâgenoscope.cns.fr. Web : www.genoscope.cns.fr. Web : www.genoscope.cns.fr. Web is trand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 4537.r.

For more information about this cluster, see For more information about this cluster, see Liocation/Qualifiers
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/clone_lib="Homo sapiens PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/clone_lib="Homo sapiens the primed hote="Vector: pCMVSPORT_6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BX459083 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE012YB13 5-PRIME, mRNA sequence.
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Catarrhini, Hominidae, Homo.
                                                                                                       721 ATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGTAACAT
                                                                                                                                                                                                                                                                                781 ACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAAGGGATAGAAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        841 CAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG
                 590 AAATGNTACACGCAGAACATGTTGAGGGAGAAAAACATTGCAACAAGAAGATGGACCCACAG
                                                                                                                                                                                                                   710 AGACCCTGGAACCTGAAGTATCTYATGAAGAAACCGAGCATAGTTACCACGTGGAAGAA
                                                                                                                                                                                                                                                                                                                                                                     481 AAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAG
                                                                                541 GAGAACCACAACAAGAGGATGATGAGTTTCTTATGGCGACTGATGTAGATGATAGATTTG
                                                                                                                                                                      AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGA
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Verte
Bukaryota; Metazoa; Chordata; Catarrhini; Hommania; Eutheria; Primates; Catarrhini; Hom
I (bases 1 to 1085)
Li, W.B. Gruber, C., Jessee, J. and Polayes, D.
Unpublished (2001)
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/organism="Homo sapiens"
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BX459083
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
Library was not normalized."
                                                                                                                                                                                            Contact: Genoscope
Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCWVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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                                                                   Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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For more information about this cluster, see
http://www.genscope.cns.fr/cdna?e=CLOBA0072C04RP1&c=4537.r.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.6%; Score 873.4; DB 5; Length 1011;
llarity 97.6%; Pred. No. 9.9e-213;
Conservative 5; Mismatches 17; Indels 0;
                                                              Bukaryota, Metazoa, Chordata, Craniata, Verte
Mammalia, Butheria, Primates; Catarrhini; Hon
1 (bases 1 to 1011)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Unil-length cDNA libraries and normalization
Unpublished (2001)
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/db_xref="taxon:9606"
                             sapiens (human)
                                                     Homo sapiens
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Isogai, T.

HI human CDNA project
Uppublished (2000)
Contact: Takao Isogai
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarau, Chiba 292-0812, Japan
Helix Research CDNA project, 5'- & 3'-end one pass sequencing: Helix
Fax: 81-438-52-3975
Fax: 81-438-52-3975
Fax: Bl-438-52-3975
Fax: Bl-438
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                                                                                                  Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 859)
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Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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/cell_line="WPC"
/coll_line="WPC"
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/coll_line="WPC"
/coll after 2-weeks retinoic acid (RA) induction"
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33.9%; Score 787.6; DB 1; Length 859;
Best Local Similarity 96.5%; Pred. No.1e-190;
Matches 834; Conservative 0; Mismatches 25; Indels 5
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                                                   AU130952.1 GI:10991306
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the Not I and EcoRV sites of the pCMVSPORT 6 vector Library was not normalized."
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                                                                                               Length 1085;
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                                                                                            Score 834.6; DB 5;
Pred. No. 9.3e-203;
1; Mismatches 5;
                                                                                            35.9%;
ilarity 99.3%;
Conservative
                                                                                          Query Match
Best Local Similarity
Matches 837; Conserv
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CK724966 182 bp mRNA linear EST 05-AUG-2004
UI-H-ED1-axp-c-22-0-UI.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone
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Local Similarity 96.3%;
es 758; Conservative C
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E. 1 (Sases I to 930)

I. (Sases I to 930)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgap09s-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CONTACT: Robert Strausberg, Ph.D.

Email: cgap09s-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CONTACT: Robert Strayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLML at:

http://image.llnl.gov f column: 15

High quality sequence stop: 549.

Location/Qualifiers

Location/Qualifiers
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                                                                                                                                                                                                                                         GAAGTTAATCCGAGATGAAGGCCTTGCAGTGATGGATAAAGCCAAAGGTCTCTTCCTGCC 1852
                                                                                             CATGCAGAGGGTTGGGAACAAAGAGGGCATATAAGTGGTATGAGCTTGGGCACAAAGAGAGG 1672
                                                                                                                                                         /tissue_type="dorsal root ganglia"
/dev stage="adult, 36 yr"
/lab_host="DH10B"
/clone lib="Lupp&ki dorsal root ganglion"
/note="Vector: pCWV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
            CATGCAGAGGTTGGGAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCACAAGAGANG
                                                                                                                                           ACACTTIGCATCTGTCTGGCAACGCTCACTCTACAATGTGAATGGACTGAAAGCACAGCC
                                                                                                                                                                                          AATAGAATCCGGAGATCCTGGCACTGATGATGGGAGATTTTATTTCCACCTGGGGGATGC
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6177038"
                                                                                                                                                                                                                                                                                          TGAGGATGAAACCTGAGGGAAAA 1876
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Homo sapiens
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                                                          (Baylor
S'-GACTAGTTCTAGATCGCGAGCCGCCCT(15)-3'. Size selected : 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."
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                                                                                                                                                                                      5
                                                                                                                                                      930;
                                                                                                                                                    Length
                                                                                                                                                                                        Indels
                                                                                                                                                  Score 719.8; DB 5;
Pred. No. 2.7e-173;
0; Mismatches 27;
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TGCTGAGTGTGACACCTAATGATGGCTTTGCTAAAGTCCATTATGGCTTCATCCTGAAGG 1509
                                                                                                                                                      CTGGCACTGATGATGGGAGATTTTATTTCCACCTGGGGGATGCCATGCAGAGGGTTGGGA 1629
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I (bases I to 689)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and LIC Frontier Korean EST Project 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BM790814 689 bp mRNA linear EST 05-MAR-2002
KrEST0070696 S21SNU520 Homo sapiens cDNA clone S21SNU520-16-C08 5',
mRNA sequence.
BM790814
                                                                                    238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1870 GGGAAAAAGGGGACTGGAGCCAGTTCACGCTGTGGCAGCAAGGAAGAAATGAAA 1926
                                                                                                                                                                                                                                                                                                                                                                                              297 ACAAAGAGGCATATAAGTGGTATGAGCTTGGGCCACAAGAGAACACTTTGCATCTGTCT
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Notes Research Institute of Bioscience & Biotechnology
S2 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Fas: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 16 row: C column: 08
High quality sequence stop: 689.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Stomach"
/cell_type="Floating aggregates"
/cell_line="SNU-520"
/lab_nost="ToplOF"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="$21SNU520-16-C08"
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Homo sapiens
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BM790814
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AUTHORS
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Inpublished (1997),

Unpublished (1997),

Office of Cancer Institute / NIH

Office of Cancer Institute / NIH

Bidg: 31 RmlOAO7 Bethesda, MD 20892

Email: cgapbe-remail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html

Seq primer: M13 FORWARD

POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  // Organism="Homo sapiens"
// mol type="mRNA"
// mol type="mRNA"
// do_xref="taxon:9606"
// clone="UT-HED1-axp-c-22-0-UI"
// tissue type="Chondrosarcoma"
// dev stage="halle"
// lab_host="DH10B (Life Technologies)"
// clone="Lip="NCI_CGAP_EDI"
// clone="Organ: Left Pubic Bone; Vector: pT7T3-Pac
// site 2: Not I: NOI CGAP_EDI is a normalized—CDNR library
// containing the following tissue(s): Chondrosarcoma cell
line CSs. The library was constructed according to
Bonaldo, Lemnon and Soares, Genome Research, 6:791-806,
oligo-dT primer containing a Not I site. Double stranded
cDNR was ligated to an EcoR I site. Double stranded
oligomucleoride used to prime the synthesis of conted between the Not I site and the (dT)18 rail. The
sequence tag for this library is GCTCAAGGCT.
TAG_IBBUI-H-BNI TAG_IBBUI-H-BNI
TAG_ISBUI-H-BNI
TAG_
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                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dasses 1 to 78).

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           658
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Pred. No. 1.9e-167;
0; Mismatches 7; Indels
UI-H-BD1-axp-c-22-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cocation/Qualifiers
                     CK724966
CK724966.1 GI:42535838
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Best Local Similarity 98.9%;
Matches 709; Conservative 0
                                                                                               sapiens (human)
                                                                                                                        Homo sapiens
                                                                                               Ношо
                                                                       EST.
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/Colone 11D="SZESNUSZE" /
// CLONE 11D="SZESNUSZE" /
// CLONE 11D="SZESNUSZE" /
// Site 2: NOT1; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intext mRNA was ligated with DNA-RNA linker including ECOR is site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The cDNA vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coll DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coll TOplOF' by electroporation method. The CDNA libraries constructed by this method are full-length enriched CDNA library."
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                                                                                                                                                                                                                                                                                                                                                               Length 689;
                                                                                                                                                                                                                                                                                                                                                                 29.6%; Score 689; DB 4; Length 68
llarity 100.0%; Pred. No. 2e-165;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGACTGGAGCCAGTTCACGCTGTGGCAG 1907
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                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            689;
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_7914661 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6147375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 72"
/note="Ocygan: skini", Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (Dases 1 to 918)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAGAGAGATGTACTTCAGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                            Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI3477 row: b column: 16
High quality sequence stop: 634.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 918;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 667.8; DB 5;
Pred. No. 6.2e-160;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:6147375"
                                                                     BU166117.1 GI:22680069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.7%;
Local Similarity 91.3%;
les 775; Conservative
                                                                                                   Homo sapiens (human)
                                 5', mRNA sequence.
BU166117
                                                                                                                    Homo sapiens
                            AGENCOURT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
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I (bases 1 to 76);

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Enomics

National Cancer Enstitute / NIH

Bldg. 31 Rml0A07 Bethesda, MD 20892

Email: Gappbe-r@mail.inih.gov

Tissue Procurement: Irene Ginis and Mahendra Rao, NIA

CDNA Library Preparation: Yulan Piao and Minoru Ko

CDNA Library Preparation: Yulan Piao and Minoru Ko

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC c

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/uncte="Vector: pCMV-Sport6; Site 1: Not1; Site 2: Sal1; /note="Vector: pCMV-Sport6; Site 1: Not1; Site 2: Sal1; This is a long-transcript enriched CDNA library (Genome Res. 11: 1553-1558 (2001). [PMID: 11544199] From WA01 cell line . Undifferentiated human ES cell line WA01 was obtained from Wiccall Research Institute. Inc., Madison, Wi, cultured according to their instructions on MEF feeders. They formed round colonies with defined edges and were positive for alkaline phosphatase, SERA-4, OCT3, OCT4, REX1, OTF, TERT, SOX2, CX43 and CX45. They are negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLT3, SERA-1, TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days after plating), the ES cells from 4 X cm dishes were treated with 1 mg/ml collegenase, type IV (Invitrogen/GIECO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with TRIZOl Reagent from Invitrogen. Protocol ref Genome Res. 11: 1553-1558 (2001). [PMID:1154199]) Double-stranded cDNAs were synthesized with an oligo(dT) primer [Invitrogen: STAA4199]) Double-stranded cDNAs were applied by ethanol-precipitation. The CDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal-4. For 25 cycles. The products (Texara) with a primer Sal-4. For 25 cycles. The products were purified by phenol/chloroform extraction and separated from kree linkers by Centricon-100 column. The cDNAs were adgested with Sal and Not! enzymes and cloned into Sal1/Not! site of about 3.6kb."
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28.3%; Score 657.6; DB 6; Length 7 97.6%; Pred. No. 2.4e-157; .ive 0; Mismatches 16; Indels Local Similarity 97.6 es 677; Conservative

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AGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGATGAGTTTCTTATGGCGACTGA TGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAG 132 584

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TTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGATGTC 192 644

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ACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCACC 884

944 AGAAACAAATAGAAAAAGAGATGATCGAGAACAAAAGCAAAAGTTAAGAAAAAAAA	552 AGAAACAAATAGAAAAACAGATGATCCAGAACAAAAAGCANAAGTTAAGAAAAAAGAAGCC 611	1004 TAAACTITIAAAIRAAATITGATAAGACIAITAAAGCIGAACTIGAIGCIGCAGAAAAACI 1063	612 TAAACTITTANATAAATTIGATAAGACTATTAAAGCTGAACTIGATGCTGCAG-AAAACT 670	1064 CCGTAAAAGGGGAAAAATTCAGGAAGCAGTGAAT 1097	671 CCGTAAAGGGGAAAATTGAGGAGCAGTGATGCAT 704
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SUMMARIES

Description	Aaf89811 cDNA enco		Ada00640 cDNA enco	Adp23914 PRO polvp	Adr97347 Human ASP	Ad156257 Bovine CD	Abx04178 Human mRN	Adp24208 PRO polyp	Aaz23609 Human lab	Abk39743 cDNA enco	Aca12072 Human lun	Aca03258 Lung canc	Adh47310 Human lun	Adi21229 Human lun	Aca92448 DNA encod	Acn88788 Breast ca	Ach47067 Human inf	Abg59507 Human col	Adt94758 Colon can	Abl10339 Drosophil
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Diagnosing malignant neoplasm in a mammal, involves contacting mammalian sample with antibody that binds to human aspartyl beta-hydroxylase polypeptide to form antigen-antibody complex and detecting the complex.

The present sequence encodes a human aspartyl (asparaginyl) beta-hydroxylase (HAAH) enzyme. Epidermal growth factor (EGF)-like domains of

Disclosure; Page 6-7; 76pp; English.

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polypeptides are hydroxylated by HAAH enzymes. HAAH is used in the method of the invention. The specification describes a method for diagnosing a malignant neoplasm in a mammal. The method comprises contacting a body fluid with an antibody which binds to HAAH polypeptide under complex forming conditions, and detecting the antigen-antibody complex. The method is useful for diagnosing and prognosing a malignant neoplasm in a bodily fluid e.g. central nervous system (CNS) derived body fluid, blood, where the neoplasm is derived from endodermal tissue and is selected from concer, breast cancer, practice cancer, liver cancer, cancer of bile ducts, and cancer of the CNS. HAAH antibodies, linked to a cytotoxic agent, are useful for killing tumour cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue of
                                                                                                                       ATGAAAATGCCTGCAAAGGAGCTCCTAAAACCTGTACCTTACTAGAAAGTTCCCCGAGA
          GGCCGCACACAGGCCCCACAAACTGCAGGCTCCGAATGCACCTGGGCTTGGTGATTCCCA
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                                       CAACAGGATGCAGAAGAGACAGATCAAATATTCCATCATGCACCCCGGGACTCACGTGT
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(DMON/) DE LA MONTE S M.
(DEUT/) DEUTCH A H.
(GHAN/) GHANBARI H A.
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The invention relates to diagnosing a neoplasm and inhibiting tumour of growth in a mammal. Using an antibody that binds to human aspartyl (asparaginyl) beta-hydroxylase (HAAH). Diagnosing a neoplasm comprises of in level of antibody binding at tissue site compared to the level of intibody binding at tissue site compared to the level of intibody binding at tissue indicates the presence of a indicate antibody conjugated to a cyclotoxic agent to a mammal. Conspaints terring the antibody conjugated to a cyclotoxic agent to a mammal. Involves administering the antibody conjugated to a cyclotoxic agent to a mammal. Dry administering to the mammal and included are a method of conferring an immune response to a tumour cell in a mammal, by administering to the mammal and HAAH-specific immune response in a mammal, by administering to the mammal polypeptide, or its degenerate variant), a fragment of HAAH-comprising an extracellular domain and lacking a cytoplasmic domain of HAAH, and the polypeptide, or its degenerate variant), a fragment of HAAH, and the strangent which binds to HAAH (where the antibody is FBSO, 685, 5C7 or its) a mybridoma cell line chosen from Mybridoma FBSO, 4386A, HAISCA and HAA19B, and a fragment of HAAH which lacks enzymatic activity or alpha-ketogluterate binding domain and epidermal growth factor (EGF)-like domain. The methods are useful for diagnosing malignant cor haemangloma) in a mammal, for conferring immune response to a pararreatic carcinoma cell and for inducing a HAAH-specific immune response in a mammal, for conferring immune response to a parain tumour call (e.g. glioma, glioblastoma, astrocytoma cell original manger conferring immune response in a mammal. For cancer and cancer, phorestelic carcinoma cell and for inducing a HAAH-specific immune ceponse in a mammal for diagnosing neplasms derived from endodermal tissue, e.g. colon cancer, phorestelic carcinoma cell conferring cancer of the bile duces of cancer. Indivarse and cancer of the bile duces of cancer indiagnosing neglement seq
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mammal with detectably-labeled antibody which binds to
(asparaginyl) beta-hydroxylase.
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0; Mismatches
                                                              Example 1; Page 4-5; 34pp; English.
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Best Local Similarity 100.0%;
Matches 2324; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for inhibiting tumour growth in a mammal. The method comprises administering to the mammal a compound, which inhibits the expression or enzymatic activity of a human aspartyl (asparaginyl) beta-hydroxylase (HAAH) The compound may inhibit HAAH hydroxylation of a NOTCH POlypeptide. In particular, the compound may inhibit hydroxylation of an epidermal growth factor (EGF)-like repeat sequence in a NOTCH polypeptide. The methods are useful for inhibiting tumour growth or killing tumour cells, or for diagnosing or prognosticating a malignant neoplasm. In particular, the tumour or neoplasm is colon cancer, breast cancer, pancreatic cancer, liver cancer, system (CNS). The present sequence encodes HAAH.
                                                                                                                                                                                                                                                                            Inhibiting tumor growth or killing tumor cells (e.g. cancer of the colon, breast, pancreatic, liver or the central nervous system), by administering an inhibitor of the human aspartyl (asparaginyl) betahybdroxylase.
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Location/Qualifiers
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/*tag= a
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P-PSDB; ADA00639.
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ss; gene; PRO; antilnflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
                                                                                                       PRO polypeptide encoding cDNA SEQ ID NO:1092.
                         BP
                       ADP23914 standard; cDNA; 2452
                                                                                (first entry)
                                                                               18-NOV-2004
                                                    ADP23914;
              ADP2391
RESULT
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New PRO polypeptides and polymucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system. WI; Wood Van Lookeren M, Williams PM, Claim 1; SEQ ID NO 1092; 2940pp; English. 01-NOV-2002; 2002US-0423394P. 30-OCT-2003; 2003WO-US034312 gene therapy; immune system. Clark H, Schoenfeld J, GETH) GENENTECH INC WPI; 2004-419628/39. P-PSDB; ADP23915 WO2004041170-A2. 21-MAY-2004 Wu ID;

The invention relates to a novel isolated nucleic acid and the PRO polyapetide encoded by it. A protein of the invention has polyapetide encoded by it. A protein of the invention has antinilammatory, antiathetic, antiahematic; immunosuppressive, careopathic, antidiabetic, dermatological, antiabsouppressive, antiathetic, hepatotropic, and respiratory activity. A polyanclectide attiasthmatic, hepatotropic, and respiratory activity. A polyanclectide of the invention may have a use in gene therapy. The PRO polypeptide, its ogonist, antagonist, or antibody that specifically binds to the construction may have a use in gene therapy. The PRO polypeptide, its polyapetide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, civenila chronic arthritis, a spondyloarthropathy, systemic solerosis, andiamatory myopathy, Sjogren's syndrome, systemic arcidosis, autoimmune haemolytic anaemia, autoimmune chronic arthritis, partnessing disease of the central or peripheral nervous disease, a demyelinating disease of the central or peripheral nervous constemn, idiopathic demyelinating polyneuropathy, a hepatobiliary disease, inflammatory demyelinating polyneuropathy, a hepatobiliary cirhosis, granulomatous hepatitis, sclerosing cholaniary cirhosis, granulomator hepatitis, sclerosing cholaniary cirhosis, granulomane or immune mediated skin disease, a bullous skin disease, asthma, allergic rhintis, atopic dermatitis, poor disease, asthma, allergic rhintis, atopic dermatitis, poor disease, asthma, allergic rhintis, atopic dermatitis, code to hypersensitivity, urricaria, an immunologic disease of the lung, conscined disease, graft rejection or preumonitis, a transplantation associated disease, graft rejection or preumonitis, are present sequence encodes a PRO protein of graft-versus. graft-versus-host disease. The present sequence encodes a

Gaps DB 13; Length 2452; ; Sequence 2452 BP; 779 A; 507 C; 657 G; 509 T; 0 U; 0 Other; Indels 2; Score 2320.8; Pred. No. 0; 0; Mismatches 99.98; sest Local Similarity 99.9 Aatches 2322; Conservative Similarity Query Match Best Local S:

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                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to novel agents that modulates the function of human apoptosis-associated proteins specified within the specification. Specifically, it refers to a method for the identification of target genes whose expression is correlated with an early stage in the capulation of apoptosis. The present invention describes a method of contacting either candidate agents or control agents to the target genes contacting either candidate agents or control agents to the target genes and assessing the difference of binding and inhibitory activity, where the candidate agent is selected from a low molecular weight organic molecule, an antibody or fragment thereof, an antisense oligonucleotide, a small inhibitory dsRNA, or a ribozyme. As such, the compositions and associated with abnormal apoptosis in mammalian tissue, such as cancer, inflammation, autoimmune or neurodepencrative disorders. Accordingly, they exhibit cytostatic, antiinflammatory, immunosuppressive and neuroprotective activities. These may also be used for drug screening courses and in gene therapy. This polynucleotide sequence is a human the regulation of apoptosis that can be applied the activities of the regulation of apoptosis that can be
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                                                                                                                                                                                                                                                                                                                                                 Identifying an agent that modulates the function of an apoptosis-
associated polypeptide, useful for diagnosing or treating e.g. cancer,
comprises comparing the binding of the polypeptide to the candidate agent
and to a control agent.
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                                                                                                neurodegenerative disorder; cancer; inflammation; autoimmune; immunosuppressive; neuroprotective; gene therapy; ASPH; aspartate beta hydroxylase.
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Matches 2322; Conserv
                         ADR97347 standard;
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                                                                                          Human ASPH DNA,
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     CCGGAGATCCTGGCACTGATGGGAGATTTTATTTCCACCTGGGGGATGCCATGCAGA
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                                                                                        63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                              Bovine cDNA differentially expressed in MYCN activated cells SeqID
                                                                                                           bovine; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy; MYCN activated cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5358 BP; 1684 A; 1009 C; 1204 G; 1461 T; 0 U; 0 Other;
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llarity 99.9%; Pred. No. 0;
Conservative 0; Mismatches
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    BP
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ADJ56257 standard; cDNA; 5358
                                                                                                                                                                                                                                                25-FEB-2002; 2002US-00084817.
                                                                                                                                                                                                                                                                             23-FEB-2001; 2001US-0270784P.
                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                              Stuart SG, Nuchtern JG,
                                                                                                                                                                                                                                                                                                       (STUA/) STUART S G.
(NUCH/) NUCHTERN J G.
(PLON/) PLON S E.
(SHOH/) SHOHET J M.
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-635698/60.
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Best Local Similarity
Matches 2321; Conserv
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                                                       36-MAY-2004
                                                                                                                                                                                                                       26-JUN-2003.
                            ADJ56257;
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Length 2680;

Sequence 2680 BP; 854 A; 446 C; 575 G; 805 T; 0 U; 0 Other;

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2538 CAATTTAGCATGAATTCATGCAAGCTTGGGAAACTCTGGAGAGA 2581
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The invention relates to new isolated nucleic acid molecule comprising a cell not acid molecule consisting of a gene differentially expressed in cells undergoing differentiation from mesenchymal cell to a cells undergoing differentiation from mesenchymal cell to a chondroblastic phenotype, or hybridising under stringent conditions to transformed host cells, expressed polypeptides or poptide fragments of the molecule or their fragments. Also included are expression vectors, which induce differentiation of a mesenchymal cell and may be used as an identifying an agent useful in modulating mesenchymal cell and may be used as an identifying an agent useful in modulating mesenchymal cell and condition characterized by aberrant expression of a nucleic acid molecule or its expression product, a method for determining regression, progression or onset of cartilaginous tissue degeneration condition in a condition characterised by aberrant expression of a nucleic acid molecule or its expression product, a method for treating a cartilaginous tissue degeneration condition, a method for identifying a candidate agent for treating a cartilaginous tissue cartilaginous tissue degeneration condition, and a solid-phase nucleic cartilaginous tissue degeneration condition, and a solid-phase nucleic cartilaginous tissue degeneration condition, and a solid-phase nucleic card molecule array consisting essentially of a set of nucleic acid differentially expressed in developing mesenchymal cells using the cechnique of representational difference analysis, RDA), its expression conditions and agentes are useful for treating cartilaginous tissue degeneration conditions are useful for treating detrimined cardidated degeneration conditions are useful for treating deformance of regeneration or and account of a solid-phase and agentes are useful for treating derivations degeneration conditions are useful for treating deformation conditions are useful for treating deformation conditions are useful for treating deformations of archivet or fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecules capable of promoting chondrogenesis, useful for diagnosing and treating cartilaginous tissue degeneration conditions, e.g. osteoarthritis, rheumatoid arthritis, gout arthritis, or
                                                                                                                                                                                                            Human, 88; gene; skeletal growth; cartilage degeneration disorder; chondroblastic phenotype; mesenchymal cell; cartilage formation; bone formation, arthritis; osteoarthritis; rheumatoid arthritis; gout arthritis; adjuvant arthritis; arthritis deformans; antigout; infectious arthritis; osteochondrosis; RDA; antiarthritic; osteopathic; antirheumatic; antiinflammatory; representational difference analysis.
                                                                                                                                                                 Human mRNA differentially expressed in mesenchymal cells #25.
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                          ABX04178 standard; cDNA; 2680 BP
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                                                                                                                      (first entry)
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                                                                     ABX04178;
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                          5; Indels
    Score 947; DB 6; L
Pred. No. 8.8e-220;
0; Mismatches 5;
Query Match
Best Local Similarity 99.5%;
Matches 950; Conservative
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RESULT 8 ADP24208

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se; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
immunosuppressive; osteopathic; antidiabetic; dermatological;
antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
gene therapy; immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 947; DB 13; Length 2680;
Pred. No. 8.8e-220;
0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2680 BP; 854 A; 446 C; 575 G; 805 T; 0 U; 0 Other;
                                        polypeptide encoding cDNA SEQ ID NO:1386.
                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1386; 2940pp; English.
ADP24208 standard; cDNA; 2680 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.78;
                                                                                                                                        30-OCT-2003; 2003WO-US034312
                                                                                                                                                     01-NOV-2002; 2002US-0423394P.
                             (first entry)
                                                                                                                                                                                  Schoenfeld J,
                                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                        2004-419628/39
                                                                                                                                                                                                                P-PSDB; ADP24209
                                                                                                            WO2004041170-A2.
                                                                                                                                                                                                                                                   nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the invention
                                                                                              Unidentified
                                                                                                                          21-MAY-2004.
                            18-NOV-2004
                                                                                                                                                                                   Clark H,
              ADP24208;
                                                                                                                                                                                          Wu TD;
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New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
Wood WI;
    Van Lookeren M, Williams PM,
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The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antifinated by it. A protein of the invention has antifinated to, antichabetic, dermatological, antipsoriatic, antiallergic, costeopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, antiasthmatic, hepatotropic, and respiratory activity. A polymucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the agonist, antagonist, or antibody that specifically binds to the collopathic inflammatory myopathy. Signathropathy, systemic sclerosis, it is systemic arthritis, a spondyloarthropathy, systemic sclerosis, andiopathic inflammatory myopathy. Signar syndrome, systemic sclerosis, antidopathic inflammatory myopathy, Signar ansemia, autoimmune contained, thrombocytopenia, throiditis, diabetes mellitus, immune-mediated renal chsease, a demyelinating disease of the central or peripheral nervous cystem, idiopathic demyelinating polymeuropathy, Guillain-Barre syndrome, system, idiopathic demyelinating polymeuropathy, Guillain-Barre syndrome, confisease, infectious or autoimmune chronic active hepatitis, primary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Mhipple's cisease, asthma, allergic rhinitis, atopic dermatitis, food disease, asthma, allergic rhinitis, atopic dermatitis, produced sensibility prememonia, idiopathic pulmonary fibrosis, hypersensitivity, uriticaria, an immunologic disease, of the lung, consinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity.
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Best Local Similarity 99.5 Matches 950; Conservative

Query Match

Human labyrinthin cDNA

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                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel polymucleotide and polypeptide sequence for the antigen detected by the antibody MCA 44-3AG. This antigen is designated Labyrinthin (lab). Antibodies directed to the Labyrinthin (lab) are useful in diagnostic assays for cancer, e.g. to monitor the presence and amount of antibodies (this method is especially useful for accept and analyse). As the Lab gene is not tissue-specific, it that have the Lab marker). As the Lab gene is not tissue-specific, it will detect cancer regardless of which organ it occurs in. Peptides cancer and/or to treat humans with cancer. Antibody MCA 44-3A6 is able to differentiate antigens associated with adenocarcinomas. However, the conference of the antigens associated with adenocarcinomas in cancer sequence of this antigen would enhance its usefulness in cancer cancer antigens associated with settliness in cancer attigen artigen would enhance its usefulness in cancer cancer attigen expension of the polypeptide and polymucleotide sequence of this antigen would enhance its usefulness in cancer attigen sequence of this antigen recognized by the MCA 44-3A6 antibody. This sequence of the antigen recognized by the MCA 44-3A6 antibody. This sequence and the number of the polymetric and prevention. The present invention discloses the sequence and the number of the number of the method of the cancer sequence.
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                                                                                                                                                                                                                                                                                                                                                   Novel Labyrinthin polymucleotides and polypeptides used as a diagnostic marker for cancer and in anticancer vaccines.
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            Labyrinthin; human; cancer; marker; antigen; detection; antibody; MCA 44-3A6; diagnostic; vaccine; treatment; adenocarcinoma; ds.
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Best Local Similarity 98.8%;
Matches 825; Conservative (
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P-PSDB; AAY33642.
                                                                                                                                                                                                                                                                                    Radosevich JA;
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08-SEP-2000; 2000US-00658124.

26-SEP-2000; 2000US-00671325.

06-OCT-2000; 2000US-00677419.

30-OCT-2000; 2000US-00705.

13-DEC-2000; 2000US-00734657.
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                                                                                         The invention describes an isolated polynuclectide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynuclectide and/or polypeptide is useful for treating a lung cancer in a patient. The polypeptide is useful for removing tumour cells from a biological sample. The polynuclectide is also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This sequence encodes a lung tumour associated protein or protein fragment, described in the method of the invention. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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Mcnabb A;
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stimulating and/or expanding T cells specific for a tumor protein
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k TS, Bangur CS,
Clapper JD;
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98.8%; Pred. No. 1.2e-188;
iive 0; Mismatches 10;
  GR, Vedvick
Mcneill PD, C
                                                                            Claim 7; SEQ ID NO 1791; 223pp; English.
     Fanger
  Marnerakis M, Carter D, Fanger
Wang A, Fanger N, Switzer A,
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Best Local Similarity 98.8
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The invention relates to a polynucleotide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences mentioned in comprising a sequence selected from any of the 14 sequences mentioned in specification, considered in specification, considered in specification, considered in specification, considered in sequences that hybridise to 31, sequences having 75%, preferably considered in the specification of soluted and one of isolated polypeptide (comprising a sequence from any one of isolated polypeptide (comprising a sequence shaving at least 70%, concerned by the polynucleotide, or sequences having at least 70%, conferably 90% identity to a sequence encoded by the polynucleotide, and sequence concerned by the polynucleotide operably linked to an expression control sequence, a host cell transformed or transfected with the vector, an isolated antibody (or its antigen-binding fragment) that the vector, an isolated antibody (or its antigen-binding fragment) that the patient, a fusion protein comprising the polypeptide, an oligonucleotide that hybridises to 31 under moderately stringent conditions, stimulating and/or expanding T cells specific for a tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel lung cancer polynucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer.
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                                       CAGAAGTAACTGCTCCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG
ACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCA
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                                                                                                                                                                                                                                                                                  Human lung cancer-associated cDNA L979P extended sequence.
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FANGER G R.
WANG A.
SWITZER A P.
MCNEILL P D.
CLAPPER J D.
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P-PSDB; ABU69516.
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us-09-436-184-3.rng

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correctin (comprising contacting T cells with the polynucleotide, protein correcting cells, under conditions and for a time sufficient content the stimulation and/or expansion of T cells) and inhibiting the development of a cancer in a patient (by incubating CD4*+ and/or CD8*+ T cells isolated from a patient with the polynucleotide, protein or antigen presenting cells that express the polynucleotide, such that T cells proliferated T cells, and thus inhibiting the development of the proliferated T cells, and thus inhibiting the development of a cancer in the patient. The polynucleotide, protein and scills are useful in a composition for stimulating an immune response in a patient, and for cligonucleotide is useful for determining the presence of a cancer in compositions, e.g. vaccines. The polynucleotide is a set useful in pharmacentical compositions, e.g. vaccines. The polynucleotide is also useful as a probe or primer for nucleic acid hybridisation, and in the design and proteins in tunour cells. An amplified portion of tunour preparation of ribozyme molecules for inhibiting expression of tunour colls in the present sequence is a cDNA, (full length gene from a suitable planary. The present sequence is a cDNA, (full length gene from a suitable planary. The present sequence is a cDNA, (full length gene from a suitable partial) isolated from a library derived from lung tunour/cancer cells. Note: The sequence date for this patent did not form part of the printed sequence date for this patent did not form part of the printed sequence. The present did not form part of the printed sequence is a cDNA, sequence for mated in electronic format directly from the construction, but was obtained in electronic format directly from the
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0; Gaps Ouery Match 35.2%; Score 819; DB 8; Length 2442; Best Local Similarity 98.8%; Pred. No. 1.2e-188; Matches 825; Conservative 0; Mismatches 10; Indels Sequence 2442 BP; 781 A; 391 C; 512 G; 758 T; 0 U; 0 Other;

121 AGCATGGAGGACACAAAAAAAAGGGGAAATCTCGGGAACTTCATCTTCACGT 180 240 TTGTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGAGAG 300 301 ATTTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAGAGAGATCTACTTCAGAGC 360 CAGCAGTCCCGCCAGAAGAGGCTGAGCCACACTGAGCCCGGAGGAGCAGGTTCCTGTGG 420 AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG 480 AAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGAAGATGGACCCACAG 540 424 600 099 484 544 720 64 604 GGTTTATGGTGATTGCTTGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC GAGAACCACAACAAGAGGATGATGAGTTTTCTTATGGCGACTGATGTAGATGTAGATTTG GAGAACCACAACAAGAGGATGATGAGTTTCTTATGCCGACTGATGTAGATGATGATTG AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGA AGACCCTGGAACTTGAAGTATCTCATGAAGAACCGAGCATAGTTACCACGTGGAAGAGA CAGITICACAAGACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAAATCCAG 9 181 241 361 245 421 305 481 365 541 425 601 485 545 661 ò 셤 δ g ò 8 S g 성 음 δ 6 B 8 S g à 셤 ò

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           CAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide, useful for preparing a composition for treating or inhibiting development of cancer, e.g. lung cancer.
                                                                        Henderson RA, Wang T, Watanabe Y, Johnson JC, Retter MW;
Durham M, Carter D, Fanger GR, Vedvick TS, Bangur CS, Mcnabb A;
                                                                                                                                                                                                                   Lung cancer; cytostatic; vaccine; gene therapy; cancer; gene;
                                                                                                                                                                                                 Lung cancer therapyand diagnosis associated cDNA #1745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; SEQID NO 1791; 82pp; English.
                                                                                                                                           ACA03258 standard; cDNA; 2442 BP.
                                                                                                                                                                                                                                                                                                                30-JUN-1999; 99US-00446492.

15-DEC-1999; 99US-00419356.

30-DEC-1999; 99US-00416300.

06-MAR-2000; 2000US-00519642.

22-MAR-2000; 2000US-00519642.

22-MAR-2000; 2000US-00519642.

27-APR-2000; 2000US-0051841.

11-JUL-2000; 2000US-005184.

11-JUL-2000; 2000US-005184.

25-AUG-2000; 2000US-005182.

06-SEP-2000; 2000US-005182.

06-SEP-2000; 2000US-005182.

06-OCT-2000; 2000US-0057132.

06-CT-2000; 2000US-0057132.

06-CT-2000; 2000US-0057132.

06-CT-2000; 2000US-0057132.
                                                                                                                                                                                                                                                                                               10-JUL-2001; 2001US-00902941
                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-328427/31.
                                                                                                                                                                                                                                                           US2002172952-A1.
                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                22-MAY-2003
                                                                                                                                                                                                                                                                              21-NOV-2002.
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                                                     725
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The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polynucleotide associated with the compositions and methods for the therapy and diagnosis of lung cancer

Sequence 2442 BP; 781 A; 391 C; 512 G; 758 T; 0 U; 0 Other;

780 664

ATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGTAACAT

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                                                                                                                                                                                                      AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG 480
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                                                                                                                                    ATTTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAAGAGAGATCTACTTCAGAGC
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                                                                   GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTTGGTTTGATC
                                 121 AGCATGGAGGACACAAGAATGGGAAGGAGGAGGCGGACTCTCGGGAACTTCATTCTTCACGT
                                             AAGTAAGCATTTTCCTGTGGAAGAACAGCAGGAAGTACCACCAGAAACAAATAG 955
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Length 2442;
                  10; Indels
 Score 819; DB 8; I
Pred. No. 1.2e-188;
0; Mismatches 10;
   35.2%;
98.8%;
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The invention relates to novel compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer. The compositions comprise one or more lung tunnour polypeptides, immunogenic portions theref, polynucleotides that encode such polypeptides, antigen presenting cells that express such polypeptides, and T cells that are specific for cells expressing such polypeptides. The novel compositions have cycostatic and immunostimulant activity. The lung tunnour antigens can be used in the creation of a vaccine. The polynucleotides that encode the lung tunnour polypeptides can be used in gene therapy to help in the treatment of lung tunnours. This polynucleotide sequence represents a treatment of lung tunnours. This polynucleotide sequence represents a treatment of lung tunnours. This polynucleotide sequence vas not human lung tunnour cDNA clone of the invention. This sequence was not shown in the specification. It has been taken from a World Intellectual Property Organization CD ROM supplied with the specification.

TS;

Vedvick

Sleath PR Fanger GR,

ο, Ο,

Kalos N Carter I

Watanabe Y, Durham M,

Henderson RA, Wang T, Johnson JC, Retter MW, Bangur CS, Mcnabb A; WPI; 2003-468346/44.

CORI-) CORIXA CORP.

28-OCT-2002; 2002WO-US034777. 29-OCT-2001; 2001US-00017754 28-MAR-2002; 2002US-00113872

WO2003037267-A2 Homo sapiens

08-MAY-2003

New polypeptides and encoding polynuclectides, useful for diagnosing, preventing and/or treating lung cancer.

5; SEQ ID NO 1791; 258pp; English.

Example

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180

64

240 124 300 184

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AAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCCACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGTTGACTATGAGGAAGTTCTAGGAAACTAGGAATCTATGATGCTGATGGTGATGGAG
                                                                                                                                                                                                                                                                                                                                                                       ATTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAGAGAGATCTACTTCAGAGC
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                                                                                                                                                                                                                                                                 Sequence 2442 BP; 781 A; 391 C; 512 G; 758 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.8
Matches 825; Conservative
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360

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424

lung cancer; tumour; cytostatic; immunostimulant; vaccine; gene therapy;

human; clone; ss.

Human lung tumour cDNA clone, SEQ ID No 1791

(first entry)

25-MAR-2004 ADH47310;

ADH47310 standard; cDNA; 2442

RESULT 13

480

TS;

us-09-436-184-3.rng

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The invention relates to a novel isolated polynucleotide comprising a sequence chosen from any one of 40 lung tumour polypeptides or its complements, fragments or degenerate variants. The method of the invention has cytostatic applications and may be useful for detecting and treating lung cancer in a patient, as well as for inhibiting the development of lung cancer in a patient via incubating COH+ and/Or COB+ polypeptide, polynucleotide or antigen presenting cell (APC) of the invention and administering an effective amount of the proliferated T cells to the patient. The current sequence is that of the human lung cancer—related CDM, of the invention. The current sequence is not shown in the specification per se but is available on the USPTO web-site http:seqdata.uspto.gov/sequence.thml?DocID=20030211510.
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            Vedvick
                                                                            Novel polynucleotide encoding lung tumor polypeptides, useful for diagnosing, preventing and treating cancer e.g. lung cancer.
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            GR,
                                                                                                                                                                                                                                                                                                                                                              10; Indels
            Fanger
                                                                                                                                                                                                                                                                                                                                  35.2%; Score 819; DB 13; 98.8%; Pred. No. 1.2e-188; iive 0; Mismatches 10;
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          Carter
                                                                                                               Example 5; SEQ ID NO 1791; 99pp; English.
          Durham M,
                                                                                                                                                                                                                                                                                                                                                          825; Conservative
         Retter MW,
Mcnabb A;
                                          WPI; 2004-167010/16.
P-PSDB; ADJ21244.
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         Johnson JC,
Bangur CS,
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             AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAA
                                                             CAGTITCACAAGACTGIAATCAGGATATGGAAGAGATGATGTGTGTGTGAGGAAAAATCCAG
                                                                                                          ATTCCAGTGAACCAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGTAACAT
                                                                                                                                                             ACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCA
                                                                                                                                                                                                                                                                                         AAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCCACCAGAAACAAATAG 955
                                                                                                                                                                                                                                                                                                     tumour; cytostatic; lung cancer; human; ss; L979P; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human lung cancer-related extended L979P cDNA - SEQ ID 1791.
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15-OCT-1999; 99US-00413356.
17-DEC-1999; 99US-0046867.
30-DEC-1999; 99US-0046867.
06-MAR-2000; 2000US-00514642.
22-MAR-2000; 2000US-00514642.
10-APR-2000; 2000US-00546259.
27-APR-2000; 2000US-00546406.
05-JUN-2000; 2000US-00564406.
11-JUL-2000; 2000US-00564164.
11-JUL-2000; 2000US-00614124.
29-AUG-2000; 2000US-00614124.
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06-OCT-2000; 2000US-00677419.
30-OCT-2000; 2000US-00702705.
13-DEC-2000; 2000US-00705457.
03-MAX-2001; 2001US-00849626.
                                                                                                                                                                                                                                                                                                                                                                         ADJ21229 standard; cDNA; 2442
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New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, atherosclerosis, or
ATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGTAACAT 664
                            840
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                                                                                                                                                                                                                                                                                                                                                          Human; protein modification and maintenance molecule; PWMM; cancer; cell proliferation disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; allergy; inflammatory disorder; AlDS; developmental disorder; hypothyroidism; cushing's syndrome; gastrointestinal disorder; epithelial disorder; inflection; cytostatic, antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; vulnerary; antiinflammatory; thyromimetic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ramkumar J, Gorvad AE, Baughn MR, Emerling BM, Yang J, Lee SY; Tran UK, Becha SD, Duggan BM, Lee EA, Griffin JA, Li JX; Spraque WM, Hafalia AJA, Chawla NK, Lehr-Mason PM, Kable AE, Yue Marquis JP, Yao MG, Richarden TM, Tang TY, Jin P, Chien D; Marquis JP, Vab MB, Richarden SP, Blake JJ, Ho A, Zheng W;
                                                                                    CAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG
                                                      ACCAAGICIATGAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCA
                                                                                                   ACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCA
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                                                                                                                                            Claim 5; Page 306; 311pp; English.
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25-OCT-2001; 2001US-0335703P.
09-NOV-2001; 2001US-0348887P.
28-NOV-2001; 2001US-0334145P.
06-DEC-2001; 2001US-0337451P.
14-DEC-2001; 2001US-0340584P.
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The present invention relates to the isolation of human protein modification and maintenance molecules (PWMM), and the polymucleotide sequences encoding them. A total of 40 PMMM polypeptides (designated PMMM - 1 to PMMM-40) are disclosed. The sequences of the invention are useful for diagnosing a condition or disease associated with the expression of PMMM in a subject, preparing a polyclonal or monoclonal antibody, and

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generating an expression profile of a sample containing the polynucleotides. The diseases or conditions associated with decreased expression or overexpression of Phym are cell proliferation disorders (e.g. cancer, atherosclerosis), neurological disorders (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory disorders, (e.g. AIDS, allergies), developmental disorders (e.g. hypothyroidism, Cushing's allergies), gastrointestinal or epithelial disorders, and infections. The Phym polypeptides or their fragments are useful in screening compounds for effectiveness as agonists or antagonists of the polypeptides, or in altering the expression of the target polynucleotide and compounds specifically bind to, or modulate the activity of the polypeptide. ACA92416-ACA92455 encode the human PWMM polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----CAGATTCCAGTGAACCAGTAGAAGATGAAAGATTGCACCATGATACAGAT
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	17	617.6	26.6	3110		US-10-198-846-9938	equence 9938
	18	464.6	20.0	502	0	US-09-918-995-34279	Sequence 34279, A
υ	19	416.2	17.9	099	н	US-09-969-034-3202	equence 3202
	20	364.4	15.7	366	7	US-10-242-535A-25661	Sequence 25661, A
	21	364.4	15.7	366	7	US-10-085-783A-25661	equen
	22	317	13.6	495	4	US-10-066-543-277	equence 277,
	23	170.6	7.3	1382	7	US-10-443-622-24	equence 24,
	24	153.2	9.9	161	9	US-10-029-386-26964	equence 2696
υ	25	153.2	9.9	592		US-10-029-386-13264	Sequence 13264, A
	56	135	5.8	191	7	US-10-242-535A-2707	2707
	27	135	5.8	191	7	US-10-085-783A-2707	2707
υ	28	127.4	5.5	583		US-09-969-034-3266	3266
	29	96.8	4.2	671		US-09-991-936-1528	1528
	30	84.2	3.6	554	ы	US-10-101-487-69	69
	31	83.4	3.6	554	13	US-10-101-487-106	106,
	32	82.8	3.6	522	13	US-10-101-487-71	Sequence 71, Appl
	33	82.8	3.6	530	13	US-10-101-487-73	73,
υ	34	78.4	3.4	720	13	US-10-101-487-76	Sequence 76, Appl
	35	78.2	3.4	720	13	US-10-101-487-74	74,
	36	78	3.4	450	13	-027-632-28	equence 2825
υ	37	78	3.4	450	17	-027-632-282	2825
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Sequence 3, Application US/09903248
; Sequence 3, Application US/09903248
; Patent No. US20020102263A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: Tace, Medim
; APPLICANT: Tace, Medim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; PILE REPRENCE: 2.486-0.32 DIVS;
; CURRENT APPLICATION NUMBER: US/09/903,248
; CURRENT FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 23.24
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100.0%; Score 2324; I
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2324; Conservative 0; Mismatches
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                                                    ## Sequence 3, Application US/09859604

## Sequence 3, Application US/09859604

## Sequence 1, Application US/09859604

## Septicant: Wands, Jack R.

## APPLICANT: Wands, Jack R.

## APPLICANT: Glanbari, Hossein A.

## APPLICANT: Deutch, Alan H.

## TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS

## TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS

## CURRENT FILING DATE: 2001-05-17

## PRIOR PILING DATE: 1999-11-08

## NUMBER OF SEQ ID NOS: 13

## SEQ ID NO 3

## LENGTH: 2324
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TYPE: DNA
ORGANISM: Homo sapiens
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SOFTWARE: Patentin Ver. 2.1
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LENGTH: 2324
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CATCTGTCTGGCAACGCTCTACAATGTGAATGGACTGAAAGCACAGCCTTGGTGGA
                   CAACAGGATGCAGAAGAGGACAGATCAAATATTCCATCATGCACCCCGGGACTCACGTGT
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; Sequence 3. Application US/09903199
; Patent No. US20020122802A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
APPLICANT: Ince, Nodim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REPREMENTE: 12001-07-11
; FILE REPERENT APPLICATION NUMBER: US/09/903,199
; CURRENT FILING DATE: 2001-07-11
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SED ID NOS: 9
; NUMBER OF SED ID NOS: 9
; NUMBER OF SED ID NOS: 9
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11arity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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1. CONTINUED CONTRACTOR CONTRACTO	1081 TTGAGGAAGCAGTGAATTAAAGAACTAGTACGCAAATACCCTCAGAGTCACCAGG 1140 1141 CAAGATATGGGAAGGCCAGTGTGAGAGACTAATAGCTGAGAGAGA	1321 GAGGITCCCIGCTIACCCTGCÁGAGATAGTICAÁCTAÍTTCCCÁAÍGÁTACTTCTÍTÁA 1380 1381 AAAATGACCTTGGCGTGGGATACCTCTTGATAGGAGATAATGACAATGATAAGAAGATTT 1440 1381 AAAATGACCTTGGCGTGGGATACCTCTTGATAGGAGATAATGACAATGCAAAGAAAG		1561 CCGARGATCCTGGCACTGATGATGGGGGGGTTTTATTTTCCACCTGGGGGGTGCCATGCAGG		1741 CCCCAAAGAGGGGTACACAGAGTTAGTAAGTCTTTAGAAAGACTGGAAGTTAA 1800	1801 TCCGAGATGAGGCCTTGCAGTGATAAAGCCAAAAGCTCTTCTTCTTTTTTTT	1921 ATGAAATGCCTGCAAAGGAGCTCCTAAAACCTGTACTTACT			2101 AGGAAGGCTGCAAGATTCGATGTGCCAACGAGCCAGGACCTGGGAGGAAGGCAAGGTGC 2160	2161 TCATCTTTGATGACTCCTTTGAGCACGAGGTATGGCAGGATGCCTCATCTTTCCGGCTGA 2220 [
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us-09-436-184-3.rnpb

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1 CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCG 60		121 AGCTIGGAGGACACAGATGTGGAGGAGCGGACTTCTTCTTCTTCTTCTTCTTCTTCTTTCT	181 GGTTTTATGGTGGTTGGTGGGGGGTGTGTTTTTTTTTT	241 TIGITGACTATGAGGAAGTICTAGGAAAACTAGGAATCTATGATGCTGATGGAGGAG 300 301 ATTIGATGTGGATGATGCCAAAGTTTAATAGGACTTAAAGAGAGATTTAATAGGACTTAAAGAGAGATTTAATAGGACTTAAAGAGAGATTTAATAGGACTTAAAGAGAGATTTAATAGAGAGAG	301 ATTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTTAAAGAGAACTACTTCTGGAGC 360 361 CAGCAGTCCCGCCAGAAGAGGCCGAGAGCCACACAGAGCCAGAGGAG	361 CAGCAGTCCGCCAGAAGAGCTGAGCCACACATGAGCCCGAGGAGAGTTCTGTGG 420 421 AGGCAGAACCCCGAAATATCGAAGAGAAGAAGAAGAAATTCAGTCCCTTCTCCATG 480	421 AGGCAGAACCCCAGAATATCGAAGATGAAGAAGAAGAAGAAGAATTCATTC	481 AATGGTACACCACAACATGTTGTGTGTGTGTGTGTGTGTG	541 ĠAGAACCACAACAAGGATGATGATGTTTTTTTTTTTTGGCGACTGATGTTGATGATTTT 600 601 AGACCCTGGAACTGAAGTATCTCATGAAGAACGAGCGATAGTTACCACGTGGAAGAGA 660			781 ACCAAGTCTATGAGGAACAAGGGTATATGAACCTCTAGAAAATGAAGGGTAGAAATCA 840 	841 CAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG 900 	901 AAGTAAGCATTTTTCCTGTGGAAGAACAGGAAGTACCACCAGAAACAAATAGAAAA 960 	961 CAGATGATCCAGAACAAAAGCAAAAGTTAAGAAAAAGAGCCTAAACTTTTAAATAAA	1021 TIGATAAGACTATTAAAGCIGAACTIGGAGAAAAACTCCGTAAAAGGGGAAAAA 1080 	1081 TTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAG 1140
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	180	GCCTGAGGATG GCCTGAGGATG		OY 1921 ATGAAAATGCCTGCAAAGGAGCTCCTAAAACCTGTACCTAGAAAAGTTCCCCGAGA 1980 DD 1921 ATGAAAATGCCTGCAAAGGAGCTCCTAAAAACCTGTACTAGTAAAAAGTTCCCCGAGA 1980	Oy 1981 CAACAGGATGCAGACGATCAAATATTCCATCATGCACCCGGGACTCACGTT 2040 Db	Oy 2041 GGCCGCACACAGGGCCCACAAACTGCAGGCTCCGAATGCACCTGGGCTTGGTGATTCCCA 2100 D 111111111111111111111111111111111111	QY 2101 AGGAAGCTGCAAGATTCGATGTGCCAACGAGACCTGGGAACGTGAAGGTGC 2160 Db 2101 AGGAAGGCTGCAAGATTCGATGTGCCAACGAGACCTGGGAGGAAGGA		Oy 2221 TATTCATCGTGGATGTGTGGCATCCGGAACTGACGAGGGAGG	Qy 2281 CAATTAGCATGAATTCATGCAAGCTTGGGAAACTCTGGAGAGA 2324 	RESULT 7 US-09-436-184-3 Sequence 3, Application US/09436184 ; Publication No. US20030031670A1	JENEKAL INFORMATION: J. APPLICANT: Wands, Jack R. J. APPLICANT: de la Monte, Suzanne M. J. APPLICANT: Ince, Nedim	APPLICANT: CATLSON, ROLf I. TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS; FILE REPERENCE: R.I. Hosp Amilgnant Neoplasms; CURRENT APPLICATION NUMBER: US/09/436,184	; CVEKENT FILING DATE: 1999-11-08 ; NUMBER OF SEQ ID NOS: 7 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 3	; LENGTH: 2324 ; TYPE: DATE T	Query Match 100.0%; Score 2324; DB 10; Length 2324; Best Local Similarity 100.0%; Pred. No. 0; M Matches 2324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1419

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TIGITGACTATGAGGAAGITCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAG 300
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                                                                                                                     APPLICANT: Suean Stuart
APPLICANT: Sharon E. Plon
APPLICANT: Jed G. Nuchtern
APPLICANT: Jed G. Nuchtern
APPLICANT: Jeason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REPERRICE: PA-0046 US
FILE REPERRICE: PA-0046 US
CURRENT APPLICATION NUMBER: 60/270, 784
PRIOR APPLICATION NUMBER: 60/270, 784
PRIOR APPLICATION NUMBER: 2001-02-25
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PERL Program
SEQ ID NO 63
                                            3;
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NAME/KEY: misc feature
CTHER INFORMATION: Incyte ID No. US20030119009A1
US-10-084-817-63
                                                                                                                                                                                                                                                                            Score 2319.2;
Pred. No. 0;
0; Mismatches
                                                                                    RESULT 8
US-10-084-817-63
Sequence 63, Application US/10084817
Publication No. US20030119009A1
GENERAL INFORMATION:
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Best Local Similarity 99.9%;
Matches 2321; Conservative
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481 AAATGGTACACGCAGAACATGTTGAGGAGAAGACTTGCAACAAGAAGATGGACCCACAG 540	IGGAAGAGA AAAATCCAG IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	901 AAGTAAGGATTTTTCCTGGAAGAACAGGAGGAGTACCACAGAAATAGAAAA 960 1158 AAGTAAGCATTTTTCCTGTGGAAGAACAGGAAGTACCACAGAAATAGAAAA 960 1158 AAGTAAGCATTTTTCCTGTGAAGAAGAAGAAGAAGACACACAGAAATAGAAAA 1217 961 CAGATGATCCAGAACAAAAGCAAAAGTTAAGAAAAGAAGCAGCTAAACTTTTAAATAAA		1141 CAAGATATGGGAAGGCGCAGTGTGAGGATCATTTGGCTGAGAAGGAGAAGTAATGAGG	1261 ACCTGCTGAAGCTGAGTTTGAAGCGTCGCTCAGACAGCAATTCTAGGTCATATGA 1320	1698 ÀTGÀAGÀGGTGCTGÀGTGTGACACTÀÀTGÀTGGTGTTAGAGTCCATHTATGGCTTC 1757 1501 TCCTGAAGGCACAGAACAAAATTGCTGAGAGGCCATATTTAAAGGGAGGAATAGGAT 1560 1501 TCCTGAAGGCACAGAACAAAATTGCTGAGAGCATCCCATATTTAAAGGAAGG

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publication No. US20030180747A1
GENERAL INFORMATION:
APPLICANT: HRUBAN, RALPH H.
APPLICANT: HRUBAN, PEDRAM
APPLICANT: ARGANI, PEDRAM
APPLICANT: ARGANI, PEDRAM
TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES
TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES
CURRENT APPLICATION NUMBER: US/10/269,909
CURRENT FILING DATE: 2003-10-11
PRIOR PLICATION NUMBER: 60/328,609
PRIOR FILING DATE: 2001-10-11
PRIOR PLICATION NUMBER: 60/332,754
PRIOR PLICATION NUMBER: 60/332,754
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PATENTION OF SEQ ID NOS: 87
SOFTWARE: 
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Best Local Similarity 99.5%; Pred. No. 1.3e-214;
Matches 950; Conservative 0; Mismatches 5;
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                                          Score 947; DB 16;
Pred. No. 1.3e-214;
0; Mismatches 5;
                                             Query Match
Best Local Similarity 99.5%;
Matches 950; Conservative
                  US-10-096-534-37
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APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Garter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Thomas S.
APPLICANT: McNabb, Andria
APPLICANT: McNabb, Andria
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: 210121.478C17
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FastSEQ for Windows Version 4.0
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35.2%; Score 819; DB 9; Length 244;
Best Local Similarity 98.8%; Pred. No. 3.7e-184;
Matches 825; Conservative 0; Mismatches 10; Indels
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Patent No. US20020172952A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watnabe, Yoshiniro
APPLICANT: Watnerson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedyick, Thomas S.
APPLICANT: Bengur, Chaitanya S.
APPLICANT: McNabb, Andrianya S.
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US-09-902-941-1791
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                                                                                                                                                                                                                                                                                                                            Sequence 1791, Application US/09736457
Patent No. US20020166637A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Panger, Gary
APPLICANT: Panger, Gary
APPLICANT: Retter, Marc
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
NUMBER OF SEQ ID MAF: 1864
SOFTWARE FEASTERE FASTER OF WINDOWS VERSION 3.0
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; ORGANISM: Homo sapiens
US-09-736-457-1791
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                                                                                         CAGCAGTCCCGCCAGAAGAGGCTGAGCCAACACTGAGCCCGAGGAGCAGGTTCCTGTGG
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                                    Length 2442
                                                         10; Indels
                                    Score 819; DB 9; 1
Pred. No. 3.7e-184;
0; Mismatches 10;
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Publication No. US20030054363A1
GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
                                       35.2%;
                                         Query Match
Best Local Similarity 98.8
Matches 825; Conservative
           sapiens
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US-10-017-754-1791
        , ORGANISM: HOMO
US-09-849-626-1791
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                                            ATTTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAAGAGAGATCTACTTCAGAGC
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Sequence 1791, Application US/09849626

Publication No. US20020197669A1

GENERAL INFORMATION:

APPLICANT: Banger, Gary

APPLICANT: Ranger, Gary

APPLICANT: Wang, Tongtong

APPLICANT: Wang, Tongtong

APPLICANT: Wang, Tongtong

APPLICANT: Wang, Tongtong

APPLICANT: McNeill, Patricia

APPLICANT: Clapper, Jonathan

TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR

TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

TITLE OF INVENTION: UNMERR: US/09/849,626

CURRENT APPLICATION NUMBER: 2001-05-03

NUMBER OF SEQ ID NOS: 1926

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1791

LENGTH: 2442
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US-09-849-626-1791
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                  CAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG
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| Publication No. US20030170255A1
| Publication No. US20030170255A1
| GENERAL INFORMATION:
| APPLICANT: Watanabe, Yoshihiro
| APPLICANT: Watanabe, Yoshihiro
| APPLICANT: Ralos, Michael D.
| APPLICANT: Ralos, Michael D.
| APPLICANT: Carter, Darrick, Thomas S.
| APPLICANT: Carter, Darrick, Thomas S.
| APPLICANT: Convertion Convertions AND METHODS FOR THE THERAPY
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
| TITLE OF INVENTION: AND OLAGNOSIS OF LUNG CANCER
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US-10-113-872-1791
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US-10-113-872-1791
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Best Local Similarity 98.8%; Pred. No. 3.7e-184;
Matches 825; Conservative 0; Mismatches 10; Indels
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Reter, Marca W.
APPLICANT: Marnerakis, Margarita
APPLICANT: Marnerakis, Margarita
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Vedvick, Thomas S.
APPLICANT: Worlok, Thomas S.
APPLICANT: Worlok, Thomas S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE BERERENCE: 210121.478618
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: FREESEQ for Windows Version 4.0
LENGTH: 2442
                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-017-754-1791
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March 25, 2005, 08:06:08; Search time 408 Seconds (without alignments) 9320.361 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-436-184-3 2324

l cggaccgtgcaatggcccag......cttgggaaactctggagaga 2324 Title: Perfect score: Sequence:

1202784 segs, 818138359 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SUMMARIES	
Result		Query				
No	Score	Match	Length	BB	QI	Description
-	2324	100.0	2324	4	US-09-903-248-3	Section 3 section 3
N	2324	100.0	2324	4	US-09-903-199-3	י ה
e	2324	100.0	2324	4	US-09-903-216-3	Segmence 3, Appli
4	2324	100.0	2324	4	US-09-903-063-3	, "
ď	2324	100.0	2324	4	US-09-859-604-3	ה ה
9	823.8	35.4	2442	ო	US-09-040-485-1	Segmence 3, Appli
7	819	35.2	2442	4	US-09-702-705-1791	1,5
60	819	35.2	2442	4	US-09-736-457-1791	
o	819	35.2	2442	4	US-09-671-325-1791	1791
10	819	35.2	2442	4	US-09-659-521-1	1 200
c 11	539.8	23.2	926	4	US-09-949-016-3447	
c 12	153.2	9.9	74730	4	US-09-949-016-15189	
++1	88.8	3.8	5746	4	US-09-949-016-16453	
		3.4	601	4	US-09-949-016-122372	Semience 199375
		3.3	7218	Н	US-08-232-463-14	
16		3.2	3095	9	5231168-1	Datent No 5231160
		3.2	3095	9	5231168-1	
c 18	74.4	3.2	601	4	US-09-949-016-122387	_
19		2.9	3337	Н	US-08-072-610-1	
20		2.9	3337	7	US-08-719-822B-1	ì
21	67.4	2.9	3337	m	US-09-092-458-1	Sequence 1. Appli
22	67.	2.9	3337	4	US-08-719-821C-1	ì -
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Matches 2324; Conservative 0; Mismatches 0; Indels 0;

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Sequence 193, App Sequence 191, App Sequence 189, App Sequence 185, App Sequence 187, App Sequence 1870, A Sequence 8, Appli Sequence 6, Appli Sequence 6, Appli Sequence 1318, App Sequence 1318, App Sequence 1318, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli	
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CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/436,184
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3
LENGTH: 2324
                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 2324; Conservative 0;
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CORGANISM: Homo sapiens
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   ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF FILE REPERENCE: 21486-032 DIV3
; CURRENT APPLICATION NUMBER: US/09/903,063
; CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PATENTIN VET: 2.1
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Patent No. 6815415
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
APPLICANT: de la Monte, Suzanne M.
APPLICANT: ce la Monte, Suzanne M.
APPLICANT: Carlson, Rolf I.
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                                                                       AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGA
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Retter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Pan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: Liqun
APPLICANTION: Liqun
APPLICANT: Retter
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98.8%; Pred. No. 1.6e-224;
iive 0; Mismatches 10;
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Patent No. 6504010
GENERAL INFORMATION:
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Best Local Similarity 98.8
Matches 825; Conservative
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US-09-702-705-1791
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                   ENCODING A NOVEL MARKER FOR
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,485
FILING DATE: 17-MAR-1998
CLASSIFICATION: 530
                TITLE OF INVENTION: A GENE ENCODING A NOVEL MARKER TITLE OF INVENTION: CANCER NUMBER OF SEQUENCES: 9 CARRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: STREET: NBC Tower - Suite 3600, 455 N. Cityfront STREET: Plaza Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.4%; Score 823.8; DB 3; llarity 99.2%; Pred. No. 6.8e-226; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MARTIN, Alice 0.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 8998,
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEPHONE: 312-321-4209
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2442 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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Matches 828; Conserv
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STATE: Illinois
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LOCATION:
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Sequence 1791, Application US/09671325

Patent No. 6667154

GENERAL INFORMATION:

APPLICANT: Mang, Tongtong

APPLICANT: Lodge, Michael A.

APPLICANT: Fanger, Gary

APPLICANT: Vedvick, Ton

APPLICANT: Carter, Darrick

APPLICANT: Retter, Marc

APPLICANT: Fan, Liqun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
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Sequence 1791, Application US/09736457

Patent No. 650948

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur. Chaitanya S.
APPLICANT: Bangur. Chaitanya S.
APPLICANT: Ranger. Gary
APPLICANT: Retter, Marc
APPLI
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Pred. No. 1.6e-224;
0; Mismatches 10;
FILE REFERENCE: 210121.478C12;
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26;
NUMBER OF SEQ ID NOS: 1825;
SOFTWARE: FASISEQ for Windows Version 3.0;
SEQ ID NO 1791
LENGTH: 2442
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nilarity 98.8%;
Conservative 0
                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
US-09-671-325-1791
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Best Local Simil
Matches 825; (
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                                         SUBMEALL INFORMATION:
APPLICANT: RADOSEVICH, JAMES A.
TITLE OF INVENTION: GENE ENCODING LABYRINTHIN, A MARKER FOR CANCE TILE REPERENCE: 21511/910557
CURRENT APPLICATION NUMBER: US/09/659,521
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: PCT/US99/05365
PRIOR APPLICATION NUMBER: 09/040,485
PRIOR APPLICATION NUMBER: 09/040,485
PRIOR FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 2442
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Pred. No. 1.6e-224;
0; Mismatches 10;
Sequence 1, Application US/09659521
Patent No. 6727080
GENERAL INFORMATION:
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98.8%;
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Best Local Similarity 98.8
Matches 825; Conservative
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                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (70)..(834)
US-09-659-521-1
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RESULT 12
US-09-949-016-15189/C
US-09-949-016-15189/C
Sequence 15189, Application US/09949016
Patent No. 6812339
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Facens Facens No. 6812339
Facens Patens No. 6812339
Facens Application: Polymorphisms in Known Genes Associated
File Reference: Clooling No. 901404
Facens Application Number: US/09/949,016
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR PILING DATE: 2000-10-20
FRIOR PILING DATE: 2000-10-30
FRIOR PILING DATE: 2000-10-30
FRIOR FILING DATE: 2000-10-30
FRIOR FILING DATE: 2000-00-08
FRIOR FILING D
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                                                         GA----AGAAACCGAGCATAGTTACCACGTCGAACAGACAG-----TTTCACAGAC 674
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                                     TITCITATGGCGACTGATGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCAT
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Best Local Similarity 98.1%; Pred. No. 7.3e-32;
Matches 155; Conservative 0; Mismatches 3; Indels 0;
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NAME/KEY: misc_feature
LOCATION: (1)...(74730)
OTHER INPORMATION: n = A,T,C or G
US-09-949-016-15189
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ORGANISM: Human
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                                                                                                                                                                                                                                                                              RESULT 11
US-09-949-1016-3447/C

Sequence 3447, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
PAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR PLING DATE: 2000-04-14

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-010-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSECEN WINDOWS Version 4.0

SEQ ID NO 3447
ACCAAGICTAIGAGGAACAAGCAGTATAIGAACCICTAGAAAAIGAAGGGAIAGAAAICA 840
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                         841 CAGAAGTAACTGCTCCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG
                                                                                                              cch 23.2%; Score 539.8; DB 4; Length 956; al Similarity 83.3%; Pred. No. 1.7e-144; 782; Conservative 0; Mismatches 37; Indels 120; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    901 AAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCACCAGAAACAATAG 955
                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3447
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1490 carcactgraatraccratcrargcaagragarraaagagaragaagarriggrackrrr 1431
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                                                 268 AGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATGAAAT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  759 CATGATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.3%; Score 77.2; DB 1; Length 7.2%; Pred. No. 9.6e-11;
tive 238; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                       485 GGTACACGCAGAACATGTTGAGGGAGAAGACTTGC 519
                                                                                                                                            208 GGTACACGCAGAACATGGTATGAATTAAAATCTGC 174
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
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                                                                                                                                                                                                                                                                       Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Conservative 238;
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 31; Conserv
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US-08-232-463-14/c
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/ Sequence 122372, Application US/09949016

/ Sequence 122372, Application US/09949016

/ Sequence 122372, Application US/09949016

/ Sequence 122373, Application US/09949016

/ Sequence 122373, Application US/09949016

/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

/ CURRENT PILITGATION NUMBER: 60/241,755

/ PRIOR FILING DATE: 2000-10-20

/ PRIOR PELICATION NUMBER: 60/231,768

/ PRIOR PELICATION NUMBER: 60/231,498

/ PRIOR APPLICATION NUMBER: 60/231,498

/ PRIOR PILING DATE: 2000-10-03

/ PRIOR PELING DATE: 2000-09-08

/ NUMBER OF SEQ ID NOS: 207012

/ SOFTWARE: FEATSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                             FACELL NO. GENERAL INFORMATION:

APPLICAMT: VENTER, J. Craig et al.
APPLICAMT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSESSEQ for Windows Version 4.0
SEQ ID NO 16453
LENGTH: 5746
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67114 TTCTTCACGTGGTTTATGGTGATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTT 67055
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3.8%; Score 88.8; DB 4; Length 5746;
Best Local Similarity 97.8%; Pred. No. 3.8e-14;
Matches 90; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 601;
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                                                                                      67054 TGGTTTGATCTTGACTATGAGGAAGTTCTAGGTAA 67017
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US-09-949-016-16453/C
Sequence 16453, Application US/09949016
; Patent No. 6812339.
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Best Local Similarity 89.5
Matches 85; Conservative
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; ORGANISM: Human
US-09-949-016-122372
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ORGANISM: Human
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LENGTH: 601
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131	998	1251	105	1191	111	1131	117	107		
1370 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	939 CCACCAGAAACAAATAGAAAAACAGATGATCCAGAACAAAAAGCAAAAGTTAAGAAAAAG 998	1310 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	999 AAGCCTAAAACTTTTAAATTTTGATAAGACTATTAAAGCTGAACTTGATGCTGCAGAA 1058	1250 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	1059 AAACTCCGTAAAAGGGGAAAAATTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACGC 1118	RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	1119 AAATACCCTCAGAGTCCACGAGCAAGATATGGGAAGGCGCAGTGTGAGGATGATTTGGCT 1178	RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	1179 GAGAAGAGA 1188	1070 RRRATCGCA 1061
1370	939	1310	666	1250	1059	1190	1119	1130	1179	1070
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Search completed: March 25, 2005, 14:35:49 Job time : 412 secs This Page Blank (uspto)

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.2 158404 .4 855 .7 186676 .8 191	5.6 126392 9 5.6 142265 9	4.4 941 9 4.4 1254 9 2.7 2739 4 2.6 60 6	2.5 2208 6 2.5 2208 9 2.4 177614 2 2.3 1777 4	1.7 556 4 1.5 4419 1 1.5 6024 1	1.5 6629 1 1.5 168569 1	1.4 524 1 1.4 1763 1	1.4 1951 1 1.4 2617 1	1.4 2770 1 1.4 2789 1 1.4 198991 1	1.3 566 1 1.3 919 1	1.3 988 1. 1.3 1013 1	1.3 2432 1	1.3 2637 1. 1.3 158289 2	1.2 275547 2 1.2 275547 2 1.2 27567 6	1.2 252366 2	1.1 12095 10	1.0 1519 10 1.0 1680 10 1.0 2204 10	1.0 2221 10 1.0 2342 10 1.0 110000 2 1.0 110000 2	1.0 110000 8	1.0 192578 5	1.0 224556 10	1.0 23 6	1.0 2483 10	1.0 3198 10	1.0 115135 10	1.0 163122 2	1.0 207761 3	1.0 218311 2	1.0 220755 10	1.0 239875 2	0.9 855 6
20 21 22 23	C 24		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	344 354	37 C 38	39 40	4 142	0 444 45	46	48 49	51		0 0 C C C C C C C C C C C C C C C C C C	57 58		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		89 0	70	C 72			0 78 0 79			1 40 CC	1 Q n			
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: March 25, 2005, 14:35:53; Search time 9715 Seconds (without alignments) 11591.346 Million cell updates/sec	Title: Perfect score: 2324 Sequence: 1 cggaccgtgcaatggcccag	Scoring table: OLIGO NUC Gapop_60.0 , Gapext 60.0	Searched: 4708233 segs, 24227607955 residues	Word size : 0 ,	Total number of hits satisfying chosen parameters: 9416466.	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Listing first 100 summaries	Database : GenEmbl:*	2: 92_0:: 2: 92_1tg:* 3: 9b in:*	4: gb_om:* 5: gb_ov:*	6: gb_pat:* 7: gb_ph:*	8: gp p1:* 9: gp: 10: gp: *	11: gb_sts:* 12: gb_sts:*	13: gb_un:* 14: gb_vi:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Query	score Match Length DB ID	2324 100.0 2324 6 AX146795 2324 100.0 2324 9 S83325	1766 76.0 2449 9 HSU03109	895 38.5 2680 9 AF289489	684 29.4 2280 9 AF306765 640 27.5 2442 6 BD234762	9 640 27.5 2442 6 AR274038 0 640 27.5 2442 6 AR277619	1 640 27.5 2442 6 AR441744 2 640 27.5 2442 6 AR532049	3 640 27.5 2442 6 AX369081 4 612 26.3 1080 9 BC015518	5 450 19.4 2761 9 BC025236 6 315 13.6 366 6 C0680735		9 190 8.2 132868 2 AC021323

ACC90094 Homo sapi AR224468 Homo sapi ACC67781 Sequence CC65781 Sequence ACC91173 Homo sapi AF224469 Homo sapi AF224469 Homo sapi AF224469 Homo sapi AF184241 Homo sapi AF289256 Mus muscu AC192156 Mus muscu AF28949 Mus muscu AF30265 Mus muscu AF30265 Mus muscu AF30265 Mus muscu AF30261 Mus muscu AF30363 Mus muscu AC102411 Mus muscu AC10341 Mus muscu AC10341 Mus muscu AC10361 Mus muscu AC10361 Mus muscu AC11061 Mus muscu AC11664 Callithri AC11161 Mus muscu AC11664 Callithri AC116686 Callithri AC116686 Callithri AC116686 AERtus no AC09158 Mus muscu AC09154 Danio rer AC11664 Callithri AC116686 AERtus no AC09159 Rattus no

	661 CAGTTTCACAAGACTGTAATCAGGATATGGAAGATGATGTGTGTG	901 AGTAAGCATTTTCCTGTGGAAGAACAGCAGGAAGTACCACCAGAAACAAATAGAAAA 960 901 AAGTAAGCATTTTCCTGTGGAAGAACAGCAGAAGGAACCACCAGAAACTAAATAGAAAA 960 961 CAGATGATCCAGAACAAAAGCAAAAGTTAAGAAAAGAAGAGCCTAAACTTTTAAATAAA	100 TIGAGGAGGAGGAGTTTTAAAGAACTAGTAGGAAATACCTAGAGTCCACGAGTCCACGAGTCACGAGTCACGAGTCACGAGTCACGAGTCACGAGTCACGAGTCACGAGTCACGAGTCACGAGTCACGAGTCACGAGTCACGAGTCACGAGTCACGAGTCACGAGTCACGAGAAGGAAG	
9 6 9 6	6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	8 8 8 8 8 8	8 6 8 6 8 6 8	8 8 8 8 8 8 8 8
BC046342 Mus muscu BC024048 Mus muscu AJ251200 Mus muscu BC055431 Mus muscu BC064069 Mus muscu CQ598341 Sequence BC012523 Mus muscu M82885 Drosophila	IA linear PAT 31-MAY-2001 13, Vertebrata; Buteleostomi; 1ini; Hominidae; Homo. 1 and Carlson, R.I. 1 neoplasms	gth 2324; els 0; Gaps		Aicréiadciréiceirideiritaire 240 AATCTATAATGCTGATGGTGATGGAG 300 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
22 0.9 1285 10 BCO46342 22 0.9 1294 10 BCO24048 22 0.9 1387 10 MMU251200 22 0.9 1414 10 BCO55431 22 0.9 1441 10 BCO64069 22 0.9 1933 6 CQ589341 22 0.9 1938 10 BCO12523 22 0.9 2003 3 DROBARHZE1	AX146795 Sequence 3 from Patent WO0135102. AX146795 AX146795. Homo sapiens (human) Homo sapiens (human) Homo sapiens Eukaryote; Metazoa; Chordata; Craniata; V. Mammalia; Eutheria; Primates; Catarrhini; 1 amada,J.R., de la Monte,S.M., Ince,N. and Diagnosis and treatment of malignant neopi	Patent: WO 0135102-A 3 17-MAY-2001; RHODE ISLAND HOSPITAL (US) 12324	CGACCGTGCAATGGCCCAGGGTAAGAATGCCAAGAGCAGCAGCAGCAGCAGCAGCGAGCAGCGAGCAGC	181 GGTTTATGGTGATTGCTGGGGCGTCTGGACATCTGTGTCGTTTGGTTTGTTGTTGTTTGT
C 93 C 94 C 95 C 95 C 97 100	RESULT 1 AX146795 LOCUS DEPINITION ACCESSION VERSION VERSION CRYWORDS SOUNCE ORGANISM REFERENCE AUTHORS TITLE	JOURNAL FEATURES SOURCE ORIGIN Query Mat Best Loca Matches 2	\$ 6 5 6 6 6 \$ 6 7 1 1	4 4 5 6 6 6 6 6 6 6 6 6 6 7 8 8 8 8 9 <t< td=""></t<>

COMMENT Authors note differences between this sequence and that of F. Korloth, C. Gieffers, and J. Frey: Gene 150 (2), 395-399 (1994), GenBank U03109. FEATURES 1. 2.234 Averaging Interesting Continue C	/mol_type="mmxNa" /mol_type="mmxNa" /db_xref="taxon:9606" 1	/codon_start=1 /producE=*asparty1(asparaginy1)beta-hydroxylase" /protein_id="AAB50779_1" /db_xref="G1:1911652" /db_xref="G1:1911652" /translat_in="MAQRXNAKSGGNSSSGGGSGSTSAGSSSPGARRETKHGGHKNG /ktanslat_in="MAQRXNAKSGGNSSSGGGGSTSAGSSSPGARRETKHGGHKNG /ktanslat_in="MAQRXNAKSGGNSSSGGGGSTSAGSSSPGARRETKHGGHKNG /ktanslat_in="MAQRXNAKSGGNSSSGGGGSTSAGSSPGARRETKHGGHKNG /kkGGLSGTSEFTWFWIYALLGWWTSARVOWFDLUDYSERVLGKLGIYDAGDGDFDVDD /AKVLGGLSGSFTREFWFWIYALLGWMTSARVOWFDEREREPREPOVIEDERKEQIQSLLHEMVH /ktylicitisteringongongongongongongongongongongongongon	ARAN YGGEDLETAGENGY DENGENGEN SETTEBENGY BETGERENGY HYBETT SOCKNOWE HYGGED SETTEBENGY HYBETT SOCKNOWE HYGGED SETTEBENGY BEGGET STATE SOCKNOWE HYGGENGY BENGY BE SETTEBENGY BE SOCKNOWE HYGGENGY BEGGAVY BEGGAVY BELBEGT BIT TRY TAND THE SETTEMENT BY SETTEM	TUNRIBRHIGHVIPKBGCKIRCANETRIWEBGKVLIFDDSFBHEVWODASSFRLIFIV ORIGIN Query Match Best Local Similarity 100.0%; Pred. No. 0;	Matches 2524;	Oy 61 GCTCCGGCAGCGGTAGCACGAGCAGCAGCAGCCCGGGGCCCGGAAAA 120	121 AGCATGGAGGACACAAGAATGGGAGAAAGGGGAACTTCAGGAACTTCACGT 180		OY 301 AITIGAIGIGAGCCAAAGIIITAATAGGACTTAAAGAGAGCTCACTCAGAGC 360	361 CAGCAGTCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCCGAGGAGCAGGTTCCTGTGG	Db 421 AGGCAGAACCCCAGAATATCGAAGATGAAGAACAAATTCAGTCCCTTCTCCATG 480 Oy 481 AAATGGTACACGCAACAACATGTTGAAGAAGACATTGCAACAAGAAGATGGACCCACAG 540 Db 481 AAATGGTACACGCAGAACATGTTGAGGAGAAGACTTGCAACAAGAAGATGGACCCACAG 540	
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2352. .2449
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Direct Submission
Submitted (03-NoV-1993) Korioth F., Fakultaet fuer Chemie-Biochemie
Submitted (03-NoV-1993) Korioth F., Fakultaet fuer Chemie-Biochemie
II, Universitaet Bielefeld, Universitaetsstrasse 25, Bielefeld,
33615, Germany
                                                                                                                                                                                      PRI 30-NOV-1995
                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases I to 2249)

Korioth, Gieffers, C. and Frey, J.
Cloning and characterization of the human gene encoding aspartyl beta-hydroxylase
Gene 150 (2), 395-399 (1994)

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Human aspartyl beta-hydroxylase mRNA, complete cds.
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AF289489.1 GI:11878115
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1 (bases 1 to 2680)

1 (bases 1 to 2680)

Dinchuk, J.E., Henderson, N.L., Burn, T.C., Huber, R., Ho, S.P.,

Link, J., O'Neil, K.T., Focht, R.J., Scully, M.S., Hollis, J.M.,

Hollis, G.F. and Friedman, P.A.

Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved instead of the catalytic domain share exons with
                                                                                                                                                                                                                                                                                                                                                                       AGAAGAAATGAAAATGCCTGCAAAGGAGCTCCTAAAAACCTGTACCTTACTAGAAAAGTTC
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1 (bases 1 to 2442)
Radosevich, J.A.
Gene encoding cancer marker labyrinthine
Patent: JP 2002512005-A 1 23-APR-2002;
JAMES A RADOSEVICH
                                                                                                                                                                                                                                            323 AGTITTATTAGACTTAAAGAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGC
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Pred. No. 0;
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/producte:=junctate=""
/producte:=junctate=""
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/db_xxef="G1"1991237"
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PTGEPQQEDDEFLMATDVDDRFETLEPEVSHBETEHSYHVEETVSQDCNQDMEEMMSE
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1 (bases 1 to 2280)

Treves, Feriotto, G., Moccagatta, L., Gambari, R. and Zorzato, F. Molecular cloning, expression; functional characterization, chromosomal localization, and gene structure of junctate, a novel integral calcium binding protein of sarco(endo)plasmic reticulum membrane.
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Submission
Submitted (19-SEP-2000) Experimental and Anesthesia and Research, University of Basel, Hebelstrasse 22, Basel 4031, Switzerland
                                    AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGA
                                                                                     CAGTITCACAAGACIGTAATCAGGATATGGAAGAGATGATGTGTGAGCAGGAAAATCCAG
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AF306765.1 GI:11991236
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mol_tvpe="maxNA"
db_xref="taxNA"
/chromosome="8"
/map="8q12.1"
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PAT 10-APR-2003

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                          17-MAR-1998 US 09/040485
JAMES A RADOSEVICH
C12N15/09, COTK14/47, COTK16/18, C12P21/08, C12Q1/02, C12Q1/68//
C12P21/08, C12R1:91, C12N15/00
Gene encoding cancer marker labyrinthine
Key
CDS
Location/Qualifiers
170). (834).
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                                                                                                                                               1 Similarity 99.9%; Score 640; DE Similarity 99.9%; Pred. No. 0; 90; Conservative 0; Mismatches

    .2442
    /organism="Homo sapiens"
/mol_type="genomic DNA"
    /db_xref="taxon:9606"

    Homo sapiens (human)
JP 2002512005-A/1
23-APR-2000
11.MAR-1999 JP 2000536866
17-MAR-1998 US 09/040485
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                                                                                          Unclassified.

1 (bases 1 to 2442)
Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S., Warg, T., Bangur, C.S., Manion, J. and Fan, L. Compositions and methods for the therapy and diagnosis of lung
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                                                                                                                                                                             Patent: US 6504010-A 1791 07-JAN-2003;
Location/Qualifiers
1. 2442
/organism="unknown"
/mol_type="genomic DNA"
AR274038 2442 bp DNA Sequence 1791 from patent US 6504010.
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PAT 20-FEB-2004
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                                                                                                            Unclassified.
Unclassified.
1 (bases I to 2442)
Wangy T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,
Carter, D., Retter, M.W., Mannion, J. and Fan, L.
Compositions and methods for the therapy and diagnosis of lung
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Sequence 1791 from patent US 6667154.
AR441744 1 GI:42667904
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Patent: US 6667154-A 1791 23-DEC-2003;
Location/Qualifiers
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/mol_type="genomic DNA"
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Pred. No. 0;
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Best Local Similarity 99.9%;
Matches 690; Conservative 0
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Unclassified.

Unclassified.

S. Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S., Catter,D., Retter,M.W., Mannion,J., Pan,L. and Wang,A. Compositions and methods for the therapy and diagnosis of lung cancer.

VAL Patent: US 6509448-A 1/91 21-JAN-2003, Location/Qualifiers

1. 2442

/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                      GGAACTICATICITCACGIGGITIAIGGIGATIGCATTGCIGGGCGTCIGGACAICIGIA 221
                                                                                                                                                                                                                                                                                                                                  GATGCTGATGCTGATGGAGATTTTGATGTGCATGATGCCAAAGTTTTATTAGGACTTAAA 341
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27.5%; Score 640; DB 6; Length 2442;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 690; Conservative 0; Mismatches 1; Indels (
                      AR277619 2442 bp DNA
Sequence 1791 from patent US 6509448.
AR277619.1 GI:29711268
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                      linear
                                                                                      DNA
                                                                                                                                                                                                                                                                                                 Patent: WO 0204514-A 1791 17-JAN-2002;
CORIXA CORPORATION (US)
Location/Qualifiers
              736
                                                                                   AX369081 2442 bp Dr
Sequence 1791 from Patent WO0204514.
                                                                                                                                                                                                                                                                                                                                          1. .2442
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                                                                                                                               AX369081.1 GI:18857144
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                                                                                                                                                          Homo sapiens (human)
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Winchestified.

B 1 (bases 1 to 2442)

S Radosevich, J.

Gene encoding labyrinthin, a marker for cancer MAL Patent: US 6727080-A 1 27-APR-2004;

ES 1. coation/Qualifiers

J. catton/Qualifiers

//organism="unknown"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                             Query Match 27.5%; Score 640; DB Best Local Similarity 99.9%; Pred. No. 0; Matches 690; Conservative 0; Mismatches
AATGAAGGGATAGAAATCACAGAAGTAACTG
                                                                                      2442 bp
1 from patent US 6727080.
                                                                                                                                 AR532049.1 GI:53920638
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Sequence 1
AR532049
                                                                                                                                                             Unknown.
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JOURNAL
FEATURES
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VERSION
KEYWORDS
SOURCE
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SSEPVNEDERLHHDTDDVTYQVYEEQAVYEPLBEGIEITEVTAPPEBDNPVEDSQVIV
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                                                                                                                                                                             /db_xref="taxon:9606"
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/tissue_type="Lung, carcinoma, large cell
undifferentiated."
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                                                                                                                                                               /clone_lib="NIH_MGC_69"
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                                                                                                                                                                                                                                                                                                                                                                                       /gene="ASPH"
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/product="ASPH protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Butheria; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1080)

2 Straubberg; R.L., Feligold, E.A., Grouse, L.H., Derge, J.G., Rlaushar, R.D., Collins; F.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marushina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Stapleton, M., Soares, M.B., Gardin, T.B., Toshiyuki, S., Carninci, P., Prange C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.H., Richards, S., Mockley, K.C., Malek, J.A., Gurarane, F.H., Richards, S., Worley, K.C., Malek, J.A., Gurarane, F.H., Richards, S., Sanchez, A., Whiting, M., Sodergren, E.J., Lu, X., Gibbs, R.A., Faley, J., Helton, E., Ketteman, M., Woung, A.C., Shevchenko, Y. Butterfield, Y.S., Krzywinski, M., Touchman, J. W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Buton, M.C., Schein, J., E., Jones, S.J., Lood, Itall-length human and moule cDNA sequences of more than 15,000 full-length human and moule cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.T.-MGC Project URL: http://mgc.nci.nih.gov
On Aug 25, 2003 this sequence version replaced gi:15930166.
Contact: MGC halp desk
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CONA Library Preparation: Life Technologies, Inc.
CONA Library Preparation: Life Technologies, Inc.
CONA Library Preparation: Life Technologies, Consortium (LLNL)
CONA Library Preparation: Life Technologies, Consortium (LLNL)
Web bite:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
R. M. Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                           1080 bp mRNA linear PRI 30-SEP-2003 IMAGE:3887962), partial cds.
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                Strausberg, R. Strausberg, R. Direct Submission Submission Submitted (Ol-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002).
                                                                                                          BC015518.2 GI:34189304
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                     RESULT 14
BC015518
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PUBMED
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TITLE

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/translation="MAQRKNAKSSGNSSSGSGSGSTSAGSSSPGARRETKHGGHKWG
KRGGISGTSFFTWFWIALLGWTRYNWTRDLYDVBENLGKIGAIYDAGDGDPDVDD
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AEHETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYE
through the I.W.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 42 Row: n Column: 19
This clone was selected for full length sequencing because it massed the following selection criteria: matched mRNA gi: 14589865
This clone has the following problem: The cds is short compared to the longest cds in the locus.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GCTCCGGCAGCGCTAGCACGAGTGCGGGCAGCAGCAGCCCCGGGGCCCCGGAGAGACAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="synonyms: JCTN, HAAH, CASQ2BP1, BAH"
/db xref="LocusID:444"
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                                                                                                                                                                                                                                                           1. .2761

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/ mol_type="mRNA"

/ db xref="texon:9606"

/ clone="IMAGE:5090911"

/ tissue type="Pancreas, el

/ clone_lib="NIH MGC 42"

/ lab host="Wettor: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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/db_xref="MIM:600582"
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es 500; Conservative
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1. (bases 1 to 2761)

Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausherg, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marushana, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L.,
Staplecon, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L.,
Staplecon, M., Soares, M. B., Bosk, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schevichenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation, and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found
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Homo sapiens aspartate beta-hydroxylase, mRNA (cDNA clone
IMAGE:5090911), complete cds.
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                                                                                                                                                             778 AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGA 837
              GAGAACCACAACAAGAAGGATGATGAGTTTCTTATGGCGACTGATGTAGATGATAGATTTG 777
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                                                                                         AGACCCTGGAACTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCCACGTGGAAGAGA
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BC025236.1 GI:19263910
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Homo sapiens apples and the control of the control 
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Homo sapiens cDNA clone MGC:8727 IMAGE:5264813, complete cds.
BCO66929
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   Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                  334 GACTTAAAGAGAGATCTACTTCAGAGCCAGTCCCGCCAGAAGAGGGTGAGCCACACA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGGAGAAG 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        514 ACTTGCAACAAGAAGATGGACCCACAGGAGAACCACAAGAGAGGATGATGAGTTTCTTA 573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 CTGAGCCCGAGGAGGAGGTTCCTGTGGAGGCAGAACCCCAGAATATCGAAGATGAAGCAA
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                     Length 297;
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Best Local Similarity 100.0%; Pred. No. 2.7e-151;
Matches 297; Conservative 0; Mismatches 0;
                                                                           Patent: WO 02068579-A 17305 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Strausberg, R.
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                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 25661 12-SEP-2002;
Chondrogene Inc. (CA)
Location/Qualifiers
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Pred. No. 3.2e-161;
0; Mismatches 1; Indels
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                                                                                                                                                                366 bp DNA Sequence 25661 from Patent WO02070737.

    .366
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

CQ680735
CQ680735.1 GI:42196629
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Best Local Similarity 99.7%;
Matches 365; Conservative
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Chases to 132868)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Castle,A., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burket,G., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Choepel,Y., Eptzhugh,W., Forrest,C., Gage,D., Galagan,J., Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J., Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Karatas,A., Klein,J., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Landers,T., Lehoczky,J., Levine,R., Lieu,G., Liu,G., Looke,K., Macdonald,P., Marquis,N., McBwan,P., McGurk,A., McKernan,K., McPheeters,R., Merquis,N., Memeus,L., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K., Fierre,N., Fisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D., Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thoman,N., Talamas,J., Talamas,J., Theodore,J., Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Nyman,D., Ye,W.J., Zimmer,A. and Zody,M.

Direct Submission

All repeats sequence version replaced gi:12229503.

All repeats we refatentified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                 ACULISES 13-MAY-2001 Homo sapiens clone RP11-23M4, WORKING DRAFT SEQUENCE, 2 ordered pieces.
                                                                   335 GGTTATGGTGATTGCTGGGGGGTCTGGACATCTGTAGCTGTTGTTGTTTGATC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center clone name: 23 M 4

Sequencing vector: M13; M77815; 3% of reads Sequencing vector: Plasmid; n/a; 97% of reads Sequencing vector: Plasmid; n/a; 97% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 132571 bases at least Q10

Consensus quality: 132698 bases at least Q20
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http://ftp.genome.washingcon.edu/RM/RepeatMasker.html
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Web site. http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
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Insert size: 132768; sum-of-contigs
Quality coverage: 20.3 in Q20 bases; agarose-fp
Quality coverage: 19.5 in Q20 ba.
* NOTE: This is a 'working draft' sequence. It curre
* consists of 2 contigs. Gaps between the contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nusbaum, C. and Lander, E.
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HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens (human)
                                                                                                                                                          241 TIGITGACTATGAGGAAGTICTAG 264
                                                                                                                                                                                                                 395 TTGTTGACTATGAGGAAGTTCTAG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum
Homo sapiens, clone RP11-23M4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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                                181
                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
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AUTHORS
TITLE
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JOURNAL
                                                                                                                                                                                                                                                                                                              RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
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KEYWORDS
SOURCE
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                                                                                                                                             WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbar-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKRN)
DNA Sequencing Proye The I.M.A.B.
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web Site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Incre"Asp-B-Hydro N; Region: Aspartyl beta-hydroxylase N-terminal region. This family includes the N-terminal regions of the junctin, junctate and aspartyl beta-hydroxylase proteins. Junctate is an integral BR/SR membrane calcium binding protein, which comes from a lternatively spliced form of the same gene that generates aspartyl beta-hydroxylase and junctin. Aspartyl beta-hydroxylase the post-translational hydroxylation of aspartic acid or asparagine residues contained within epidermal growth factor (BGF) domains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 167 Row: k Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14589865. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon start=1
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GIYDADGDGDFDVDDAKVLLGLTKDGSNENIDSLEEYLNILARESSDWFYGFLSFLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AGCATGGAGGACACAAGAATGGGAGGAAAGGCGGACTCTCGGGAACTTCATTCTTCACGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 AGCATGGAGGACACAAGAATGGGAGGAAGGGGGACTCTCAGGAACTTCATTCTTCACGT 334
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                         Submitted (01-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTPFEMLEEEEESETADGVDGTSQNEGVQGKTCVILDLHNQ'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="Brain, hippocampus"
clone_lib="NIH_MGC_95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.2%; Score 213; DB 9; L
99.6%; Pred. No. 5.5e-105;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="MGC:87227 IMAGE:5264813"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Vector: pBluescript"
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Direct Submission

Bubmitted (14-FEB-2011) Whitehead Institute/MTT Center for Genome Research, 320 Charles Street, Cambridge, NA 02141, USA

Research, 320 Charles Street, Cambridge, NA 02141, USA

Bitren, B. Linton, L., Nubbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barnan, N., Bastien, V., Bloom, T., Bogualawity, L., Anderson, S., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Cooke
       Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McDherers, R., Meldrim, J., Menderis, J., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R. Rieback, M., Riley, R., Riee, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schuer, S., Schupback, R., Seamen, S., Severy, P., Scouger, C., Spencer, B., Stange-Thomann, N., Stojanovic, N. Strauss, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Voin, T., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Voin, Sembak, L., Zimmer, A. and Zody, M. J., Young, G., Zainoun, J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP11-252C19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="<30 qual SNGL region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1037, .1417)
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complement(1697, .1825)
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1826, .2120
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1960, .1969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L12758
Center clone name: 252_C_19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2255 ACCACAGCAGAGACGAGCCTTCCAGCAATTTAGCATGAATTCATGCAAGCTTGGGAAAC 2314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACU90094 158404 bp DNA linear PRI 15-MAR-2002
Homo sapiens chromosome 8, clone RP11-252C19, complete sequence.
AC090094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2135 CAGGACCTGGGAAGGCAAGGTGCTCATCTTTGATGACTCCTTTGAGCACGAGGTATG 2194
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Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 8, clone RP11-252C19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 130383: contig of 130383 bp in length
130384 132868: contig of 2385 bp in length.
Location/Qualifiers
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8.2%; Score 190; DB 2; Length 132868;
Best Local Similarity 100.0%; Pred. No. 2.7e-92;
Matches 190; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="RPCI-11 Human Male BAC"
1.103038
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130684. 132688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vector_side:right"
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2000. .2020
.note="<30 qual SNGL region"
2030. .204 qual SNGL region"
.note="<30 qual SNGL region"
2086. .2096
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complement (25788. .25920)

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complement(11277. .11584)
rpt_family="Alusx"
complement(11650. .11891)
/rpt_family="LiME1"
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/rpt_family="LIMBc"
complement (12926. ,13195)
/rpt_family="AluSg"
complement (13196. ,13833)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt family="bl.
romlement(15010. .15280)
rpt family="L1PA5"
complement(15281. .17128)
.... familv="L1"
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rpt family="FLAM C"
complement (17261. 18749)
rpt family="L1"
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:complement(26462. .26590)
/rpt_family="MIR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt family="AT rich"
complement(28241. .28452)
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family="HAL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       omplement (13820. .15009)
                                                                                                                                                                                                                                                                                                                              rpt_family="AT_rich"
0154. .10511
                                                                                                                                                                                                                                                                                          rpt_family="MIR"
0056. .10077
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0770. .10866
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2255 ACCACAGCAGCAGCAGCCTTCCAGCAATTTAGCATGAATTCATGCAAGCTTGGGAAAC 2314
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Li (Bases 1 to 855)
Lim, K.Y. Hong, C.S. and Kim, D.H.
cDNA cloning and characterization of human cardiac junctin 20432113
10974562
2 (Bases 1 to 855)
Lim, K.Y. Hong, C.S. and Kim, D.H.
Direct Submission
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8.2%; Score 190; DB 9; Length 158404;
Best Local Similarity 100.0%; Pred. No. 2.7e-92;
Matches 190; Conservative 0; Mismatches 0; Indels 0;
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complement (38380. 38821)
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complement (38074. 39178)
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Homo sapiens
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Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (Dases I to 18676)

Biren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, P., Candon, C., Manato, P., Fitzhugh, M., Gage, D., Galagan, J., Gaddyns, S., Goyette, M., Gardyns, S., Marches, C., Kamat, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kartas, A., Marchis, C., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Matchews, C., Maccarthy, M., McEwan, P., McKennan, K., McRehas, R., Matchews, C., Maccarthy, M., McEwan, P., McKennan, K., McHeeters, R., Matchews, C., Manon, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Saman, S., Severy, P., Spencer, B., Strage-Thomann, N., Stojanovic, N., Stands, J., Severy, P., Spencer, B., Strage-Thomann, N., Stojanovic, N., Stands, J., Yo, A., Wallson, B., Tregilio, J., Vessiliev, H., Viel, R., Viel, R., Willow, M., Travers, M., Travers, M., Travis, N., Trigilio, J., Vessiliev, H., Viel, R., Viel, R., Wall, R., Wo, A., Wallson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Letter, A., Challer, A., Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (28-SEP-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Sep 28, 2001 this sequence version replaced gi:15422051. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) RepeatMasker: http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
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/clone_lib="RPCI-11 Human Male_BAC"
243. .278
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complement (2155. .2456)
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3358. .4039
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/db_xref="texon:9606"
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9173. 9513
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complement (5527. .7135)
/rpt family="L2"
complement (7894. .8215)
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Center clone name: 687_K_23
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9914. 9946
/rpt_family="AT_rich"
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/rpt_family="(TG)n"
complement(1919. .21
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/rpt_family="L2"
10661. .12746
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AKTKENRKKSTNMKDVSSKMASRDKDDRKESRSSTRYAHLTKGNTQKRNG"
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Homo sapiens chromosome 8, clone RP11-687K23, complete sequence.
AC067881
       Submitted (13-JAN-2000) Life Science, Kwangju Institute of Science and Technology, Kwangju 500-712, Korea Location/Qualifiers
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1866/76)
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Mmol Lypps=mRNND

Mmol Lypps=mRNND

trisue type="heart"

112. 744

mottional sarcoplasmic reticulum protein"
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                                                                                                                                                                                                                                                                                                                                                                               protein id="AAF82246.1"
db xref="GI:8979460"
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Homo sapiens
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 2707 12-SEP-2002;
Chondrogene Inc. (CA)
Location/Qualifiers
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100.0%; Pred. No. 5.3e-62;
ive 0; Mismatches 0; Indels
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Bircen, B., Linton, L., Boubalum, C., Lander, E., Allen, N., Anderson, S. Barren, M., Bastien, V., Boquelavkiy, L., Boukhgalter, B. Brown, A. Camarata, J., Campopiano, A., Chang, J., Chospel, Y., Colangelo, M., Callymoze, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J., S., Dagge, S., Farcs, S., Ferreira, P., Fitzhugh, W., Gage, D., Gandgan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Carata, M., Hagos, B., Haefock, A., Horton, L., Hulme, W., Iliav, I., Macchan, P., McKernan, R., McCheeters, R., Matthews, C., McCarthy, M., McChean, P., McKernan, R., McRheeters, R., Mallor, J., McCarthy, M., McChan, C., McChan, P., McKernan, R., McRhang, P., Marquis, M., Matthews, C., McCarthy, M., McChan, C., McChan, M., Miloy, T., Maloy, T., Maylor, J., Moylor, J., McChan, C., McChan, M., Miloy, R., Santce, R., Schupback, R., Schupback, R., Schupback, R., Schupback, R., Schupback, R., Schupback, S., 
                                                                                     ACU91173 142265 bp DNA linear PRI 16-OCT-2002
Homo sapiens chromosome 8, clone RP11-280G9, complete sequence.
AC091173
                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Birren, B., Nusbaum, C., Lander, E., Alli, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chararo, B., Chopel, Y., Collymore, A., Cook, A., Cook, P., Deyrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galegan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Landers, T., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, clone RP11-280G9
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Birren, B., Linton, L., 1
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Homo sapiens
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                                 RESULT 25
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This sequence was finished as follows unless otherwise noted: all regions were either double-erranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare cocasion of the clone being a XAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw.; SwISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/Celagans/wormpep XX-NCH2171 3M21 is from a Cancer cell lines BACS library VECTOR: pBACe3.6_BamHI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 126392)
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Submitted (27-UU-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CBIO 15A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
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/clone_lib="Cancer Gell lines BACS"
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Center code: SC
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Contact: humquery@sanger.ac.uk
487 TACACGCAGAACATG 501
                                     121 TACACGCAGAACATG 135
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project_Information
                                                                                                                                                                                                                                                                                                                                                                                clone="RP11-280G9"
Clone_lib="RPCI-11 Human Male BAC"
...76
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1915..2073
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4833_4956
4833_10956
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6152...6606
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Center clone name: 280_G_9
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286. .1579
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501 GTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAGGAGAACCACAACAAGAGAAT
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Best Local Similarity 100.0%; Pred. No. 3.2e-59;
Matches 130; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                 family="AluJb"
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omplement(14137. .14441)
rpt_family="AluSq"
4853. .14864
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omplement(15394. .16172)
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omplement (14865. .153
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9538. .19653
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1725. 148
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1330. .11619
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1620. .11729
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1956. .18092
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family="MIR3"
rpt_family="MIR"
0946. .11255
                       rpt family="L2"
1256. .11329
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rpt_family="L2"
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.8151. .18250
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GKKDREKKVDLEKSAKTKENRKKSTNMKDVSSKMASRDKDDRKESSRSTRYAHLTKG
NTQKRNG"
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Bos taurus aspartyl (asparaginyl) beta hydroxylase mRNA, complete
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos
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2 (bases 1 to 1254)
Wetzel,GT., Ding,S. and Chen,F.
Wetzel,GT., Ding,S.
Direct Submission
Submitted (08-SEP-1999) Pediatrics Cardiology, UCLA School o
Medicine, 675 Charles E. Young Drive South, Los Angeles, CA
90095-7045, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (15-APR-1992) P.A. Friedman, Merck Sharp and Dohme
Research Laboratories, West Point, PA 19486 USA
Original source text: Bos taurus cDNA to mRNA.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (Jases 1 to 2739)
Jaj.S., VanDusen,W.J., Diehl,R.E., Kohl,N.E., Dixon,R.A.,
Elliston,K.O., Stern,A.M. and Friedman,P.A.
cDNA cloning and expression of bovine aspartyl (asparaginyl)
beta-hydroxylase
J. Biol. Chem. 267 (20), 14322-14327 (1992)
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100.0%; Pred. No. 2.4e-44;
tive 0; Mismatches 0; Indels
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aspartyl (asparaginyl) beta hydroxylase.
Bos taurus (cow)
Bos taurus
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189. .2453
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2 (bases 1 to 2739)
Friedman, P.A.
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Matches 103; Conservative
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Homo sapiens
Bakaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1254)
Maczel, CT., Ding.S. and Chen.P.
Molecular cloning of junctin from human and developing rabbit heart
20232172
10767180
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WPDIVDYSEVLARAKDFRYLLSEVLGSKLGYTVADGDGDFPDDDAKVLLEGPSGVAKR
KTRAKVKELTKEELKKEKERFRFSFRKESKDERFKKGKKEDVRKDKTADDLSSFRKESPF
GKUDREKEKVVDLEKSAKTKENRKKSTNMKDVSSKMASRDDDRKESRSSTRYAHLTKG
                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 941)
Lim, K.T., Hong, C.-S. and Kim, D.H.
Direct Submission
Submitted (13-7AN-2000) Life Science, Kwangju Institute of Science
and Technology, Kwangju 500-712, Korea
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 941)
Lim, K.Y., Hong, C.S. and Kim, D.H.
CDNA cloning and characterization of human cardiac junctin Gene 255 (1), 35-42 (2000)
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/codon start=1
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                                                                               AF224469 941 bp mRNA linear Homo sapiens junctin isoform 1 mRNA, complete cds.
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                                                                                                                                      AF224469.1 GI:8979461
                                                                                                                                                                            Homo sapiens (human)
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                                  RESULT 26
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/mol_type="mRNA"
/db_xref="taxon:9606"
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ATPase, glycoprotein.
Homo sapiens (human)
Homo sapiens
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Homo sapiens (human)
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                                                                        /trainilation="MARKNAKGGGGNSSSSSSSPTGCTSGGSSSPGARRETKQGGL
KNGRKGGLSGSSFFTWFMVTALLGVWTSVAVVWFDLDVDYEBTGJAKADFRYNLSBVLQ
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IEDBYYVEQVQSLDETYVSEPGENLPQSPRGFABELQPDDHVFVGSDADDRYEBMGTGA
VHEETEDSYHIEBTASPAYSQDMEDMMYEQENPDSSEPVVVDDAERTYQETDDVTXRD
                                                                                                                                                                YDEQDHAVDNSNTILEEPHMPPAEEQQEVPPETNKKADEPGKKGKVKKKPKLLINKFD
KTIKAELDAAEKLRKRGKIEEAVNAFEELVRKYPQSPGARYGKAQCEDDLAEKRRSNE
ILRAAIETYGBAASLEPDAPTDLVKLSLKRRSPRQOFGHGHWRGSLLTLGAUGLFDDT
ALKNDLGVGYLLIGDNDSAKVYEELSVATPNDGFAKVHYGFILKAQNKIAESIPYLK
EGIESODPGTDDGRFYFHLGDAMQRYGNKEAYRWYELGHQRGHFAS WWQRSLYNVQGL
KAQPWWTPKETGYTELVKSLERNWKLIRDEGLAAMDRTHGLFLPEDENIREKGDWSQF
                                                                                                                                                                                                                                                                                  TLWOOGRKNENACKGAPKTCSLLDKFPETTGCRRGQIKYSIMHPGTHVWPHTGPTNCR
LRMHLGLVIPKEGCKIRCANETRTWEEGKVLIFDDSFEHEVWQDAASFRLIFIVDVWH
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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             produčt="aspartyl (asparaginyl) beta hydroxylase"
protein id="AAA03563.1"
'db_xref="GI:162694"
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1.2e-20;
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Sequence 322 from Patent WO03004646.
AX771609.1 GI:32438407
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llarity 100.0%; Pred. No. 1.2
Conservative 0; Mismatches
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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CQ541435.1 GI:41507699
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/db_xref="GA:28933"
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/translation="MARGKAKEEGSWKKFIMNSEKKEFIGRTGGSWFKILLFYVIFYG
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LNIVRELEKYKOSAORDDMIFEDCGDVPSEPKERGDFNHERGERKVCRFKLEWLGNCS
GLNDETYGYKEGKPCIIIKLNRVLGFKPKPPRNESLETYPVMKYNPNVLPVQCTGKRD
EDKDKVGNVEYFGLGNSPGFPLQYYFYYGKLLQPKYLQPLAVQFTNLTMDTEIRIEC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                              O'Mahony, D.J., Byrne, D., Brayden, D., Lambkin, I. and Higgins, L. Genetic analysis of Peyers's patches and M cells and methods and compositions targeting Peyer's patches and M cell receptors Patent: Wo 3004646-A 322 16-JAN-2003; ELAN CORPORATION, Plc (IE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="unnamed protein product; put. Na/K-ATPase beta
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human Na, K-ATPase
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Location/Qualifiers
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Kawakami, K., Nojima, H., Ohta, T. and Nagano,
Molecular cloning and sequence analysis of
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Nucleic Acids Res. 14 (7), 2833-2844 (1986)
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100.0%; Pred. No. 4.3e-20;
tive 0; Mismatches 0;
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A85. 1490
Acce="pot. polyA signal"
2001. .2006
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note="pot. glycosylation site"
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                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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E C Thages 1 to 177414)

Milosavijevic,A., Sodergren,E., Csuros,M., Li,B., Jackson,A.R., Adams, C., Adio-Oduola,B., Adi-Osman,F.R., Allen,C., Alabrooks,S.L., Amaratuge,H.C., Ared,J.R., Aydle,M., Banks,T., Banck,T., Bouck,J., Benton,J., Binage,K., Burnell,R.L., Bonnin,D., Bouck,J., Benton,J., Eleva,M., Brown,B., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Eurkett,C., Burrell,R.L., Bydd,N.C., Carron,T.F., Carter,M., Cavasos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chhill,D., Chowdhry,J., Christopoulos,C., Claveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davilande,C., Claveland,C.D., Dann,A.L., Ding,Y., Dinh,H.H., Douthmate,R., Daviland,C.D., Dann,A.L., Ding,Y., Dinh,H.H., Douthmate,R., Dergand,C., Claveland,C.C., Elasting,N., Ford,J., Foster,P., Farlis,T., Ferraguo,D. Garcia,A., Earnhart,C., Edwards,C.C., Harris,C.C., Flagg,N., Ford,J., Foster,P., Farlis,T., Forraguo,D. Garcia,A., Edwards,C., Harris,R., Harris,C., Harris,C., Harris,C., Harris,C.C., Harris,C.C., Harris,C.C., Harris,H., Harlak,P., Hagles,A., Holling,B., Homsi,F., Harris,M., Harlak,P., Hawes,A., Holling,B., Homsi,F., Harris,C., Harr
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1 (bases 1 to 177614)

Csuros, M. and Milosavijevic, A.

Pooled genomic indexing (PGI): mathematical analysis and experiment
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*** SEQUENCING IN PROGRESS ***.
                                                                                                                                                                                                                                                                                                            2239 GGCATCCGGAACTGACACCACAGCAGAGGCGCAGCTTCCAGCAATTTAGCATGAATTC 2297
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ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI
2002, POME, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS: 10-28;
Springer (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
                                                                                                                                                                                                          Length 2208;
                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                   ch 2.5%; Score 59; DB 9; L
1 Similarity 100.0%; Pred. No. 4.3e-20;
59; Conservative 0; Mismatches 0;
/note="pot. polya signal"
2026. .2031
/note="pot. polyA signal"
2187. .2193
/note="pot. polyA signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC143562
Macaca mulatta clone CH250-267C14,
AC143562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS PHASE2; HTGS PGI.
Macaca mulatta (rhesus monkey)
Macaca mulatta
                                                                                                                                                                                             Query Match
Best Local Similarity
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                          misc_feature
                                                                                    misc_feature
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TITLE
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* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: The contigs are based on the application
* of the Porl michtod using the Human genome (NCBI build 31)
* as the comparative genome.
* NOTE: This is a "working draft" sequence. It currently
* consists of I contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CFU38414 1777 bp mRNA linear MAM 02-FEB-1996 Canis familiaris junctional sarcoplasmic reticulum protein mRNA, complete cds.
                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (09-APR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vincon, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Woden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Kucherlapati, R., Weinstock, G. and Gibbs, R., Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Best Local Similarity 100.0%; Pred. No. 2e-18;
Matches 56; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: LBNI
Center clone name: CH550-267C14
Center clone name: CH550-267C14
Center clone name: CH560-267C14
Chemistry: Dye-primer Bodipy: inf* of reads
Chemistry: Dye-terminator Big Dye: inf* of Consensus quality: 7315 bases at least Q40
Consensus quality: 9328 bases at least Q30
Consensus quality: 9602 bases at least Q20

    177614
/note="assembly_name:CH250-267C14.1B
CONFIDENCE:_0.67"

                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor College of Medicine
Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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/mol_type="genomic DNA"
/db_xref="taxon:9544"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9544"
/clone="CH250-267C14"
                                                                                                                                                                                                                                       3 (bases 1 to 177614)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (dog)
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VERSION
KEYWORDS
SOURCE
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Gaps

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/product="asparty1 beta-hydroxylase 4.5 kb transcript"
/protein_id="AAG40808.1"
/bortein_id="118781110"
/db xref="d1:11878110"
/translation="WAPPRGARGGGGNSSSSGGSGSGSGSPSTGSSGSSSSGARRE AKHGGHRNGRRGGISGSFFTWFMVIALLGWTSVAVVWFDLVDYEEVLGKLGVYDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF289486

Mus musculus aspartyl beta-hydroxylase 4.5 kb transcript (Asph)
mRNA, complete cds; alternatively spliced.
                                                                                                                                              /translation="Ligywisyavvwpelvdybeylgkigvydadgdgdfdyddakal
lebeggyarrkkakvkelikeelkkgkekpesrreskheerkrgkkekedsrkggki
aasdvgrrespagkkskekekaesaktkenrkkstptkdlsskwaprdtddrkesrss
nQlttlakgnshkrkw"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus. I (bases 1 to 4419)
Dinchuk, J. E., Henderson, N. L., Burn, T. C., Huber, R., Ho, S. P., Link, J., O'Neil, K. T., Focht, R. J., Scully, M. S., Hollis, J. M., Aspareyl beta - hydroxylase (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (26-UUL-2000) Applied Biotechnology, DuPont
Pharmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Asph"
/note="BAH; asparaginyl beta-hydroxylase; AspH;
alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 4419)
Dinchuk,J.E., Henderson,N.L., Burn,T.C., Hollis,G.F. and
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                                                                                                                                                                                                                                                                                        Length 556;
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                                                                                                                                                                                                                                                                                                                                                                               324
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                                                                                                                                                                                                                                                                                                                                                                               285 GCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAAAG
                                                                                                                                                                                                                                                                                        DB 4; Le
1.2e-09;
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/tissue_type="liver"
                                                                                                                                                                                                                                                                                      1.7%; Score 40; DB 100.0%; Pred. No. 1.2 :ive 0; Mismatches
                                                                               /product="cardiac junctin"
/protein_id="AAF37204.1"
/db_xref="GI:7141075"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .4419
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/chromosome="8"
'db xref="taxon:9986"
                     /tissue_type="heart"
<1. .531
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                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .4419
/gene="Asph"
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Best Local Similarity
Matches 40; Conserv
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AF289486
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Oryctolagus cuniculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Eukaryota, Metazoa, Chordata, Leporidae; Oryctolagus.

1 (bases 1 to 556)
Wetzal, Gr., Ding, S. and Chen, F.
Wolecular cloning of junctin from human and developing rabbit heart
Mol. Genet. Metab. 69 (3), 252-258 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryccolagus cuniculus cardiac junctin mRNA, partial cds.
AF198966
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2 (bases 1 to 556)
2 (bases 1 to 556)
Wetzel, G.T., Ding, S. and Chen, F.
Wetzel, G.T., Ding, S. and Chen, F.
Direct Submission (26-CCT-1999) Pediatrics Cardiology, UCLA School of Direct Submitted (26-CCT-1999) Pediatrics Cardiology, UCLA School of Medicine, 675 Charles E. Young Drive South, 3754 MRL Building, Los Angeles, CA 90095-7045, USA
Angeles, CA 90095-7045, USA
Angeles, Cardion/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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KEKTESRKENKNEERRKGKKEKEDERKDKKIADADISRKESPKGKKDREKENVGLDKS
AKAKESRKKSTNVKDASSKTASRDKDDTKEGKTSSKHTHSAKGNNQKRKN"
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                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. 1 (Dases I to 1777) Jang, L., Sanborn, K., Jorgensen, A.O. and Kelley, J. Purification, primary structure, and immunological characterization of the 26-kps caleguetrin binding protein (junctin) from cardiac
                                                                                                                                                                                                                                                     CardionOpp)

2 (Dases 1 to 1777)

Jones, L.R., Zhang, L., Sanborn, K., Jorgensen, A.O. and Kelley, J.

Direct Submission
Submitted (12-CCT-1995) Larry R. Jones, Medicine, Krannert Inst.
Cardiology, 1111 W. 10 Street, Indianapolis, IN 46202, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 TCTATGATGCTGATGGTGATGTGGTGTGTGGGATGATGTCCAAAGTTTTA 313
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.3%; Score 53; DB 4; Length 1777;
llarity 100.0%; Pred. No. 8.6e-17;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tisaue_type="heart"
89. .721
/function="calsequestrin binding protein"
                                                                                                                                                                 junctional sarcoplasmic reticulum
J. Biol. Chem. 270 (51), 30787-30796 (1995)
96107245
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="junctin"
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join(AF289205.1:1772. .2075,AF289206.1:1105. .1173,
AF289207.2:14425. 1554,AF289207.2:4438 .4512,
AF289207.2:16594. 11004,AF289207.2:19820. 12557,
AF289207.2:10948 .11004,AF289207.2:15883. 15921,
AF289207.2:16600. 16635,AF289207.2:15883. 15921,
AF289207.2:16600. 16635,AF289207.2:20179. .20223,
AF289211.1:1764 .1862,AF289210.1:4279. .4415,
AF289211.1:1764 .1862,AF289210.1:4739 .4415,
AF289211.1:1788 .555,AF289211.1:4834 .655. .>6000)
AF289211.1:1788 .555,AF289211.1:2005 .2938,1665. .>6000)
AF289211.1:1788 .555,AF289207.2:1805 .1383,
AF289207.2:1425 .1541,AF289206.1:1105 .1173,
AF289207.2:1425 .1544,AF289207.2:1883 .5527,
AF289207.2:10948 .11004,AF289207.2:12833 .15291,
AF289207.2:16600 .16635,AF289207.2:12833 .15291,
AF289207.2:16800 .16635,AF289207.2:12833 .15291,
AF289207.2:12894 .2504,AF289207.2:20179 .20223,
AF289211.1:1764 .1862,AF289211.1:4834 .4415,
AF289211.1:1764 .1862,AF289211.1:4834 .4415,
AF289211.1:1764 .1862,AF289211.1:4834 .4415,
AF289211.1:1764 .1862,AF289211.1:5805 .5938,1665 .1815)
AF289211.1:1764 .1862,AF289211.1:5805 .5938,1665 .1815)
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 6629)
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/gene="ASPH"
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gene="ASPH"
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/gene="ASPH"
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AF289487
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DEFINITION
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Matches
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GDGDFDVDDAKVLLGLKERSPSERIFPPEAETHAELEGAAPGADIQNVEDEVKEQIQ
SLAGSWYHPUPUBLEADGLAGEPCPEWEDFLTYTYDSDREEDLEGTYHEEL EDTYHYB
DTASOWHPUPUBEMPURGEPCPTYBEPLTYTYDRAVLLPHAESVRHQDYDEPVYEPSEHGV
BTASOWHPUPUBEMPURGENSDPSEAVTDAGVLLPHAESVRHQDYDEPVYEPSEHGV
BISDNIIDDSSIISEEINVASVEBQDPPPVKKKKPKLLNKFDKTIKABLDAABKLEK
RGKIEBANNARDEBLVRKYPOSPRAKYGRAQCEDDLAEKQRSNEULRRAIDABAEKLEK
PAPAPDLVKLSIKRESERQOFLGHMRGSLLTLGALVQLKYPESPTTLKNDLGYGYLLLGD
NASAKKVYEBVLANTPNDGFAKVHYGFILKAQNKTSESIPYLKNDLGYGYLLLGD
NYFLGDAMQRVGNKGAYKWFLGHKRGHFASVWQRSLYNNGGLAAQPWMTRETGYTE
LVKSLERNWILIRDEGLAWMDGKAGLFLPEDBNLARKGDWSGFTLWQCRRKTBNGCK
APKTCALLEKRESETTGCRRGOIKYSIMHPGTHWPHTGFTNCRLRMHLGLVIPKGCK
1295. . 4419
/ GADGE APAPDL
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Mus musculus aspartyl beta-hydroxylase (ASPH) gene, exon 24 and
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

Dinchuk,J.E., Henderson,N.L., Burn,T.C., Huber,R., Ho,S.P.,

Link,J., O'Neil,K.T., Focht,R.J., Scully,M.S., Hollis,J.M.,

Hollis,G.F. and Friedman,P.A.

Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
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Henderson,N.L., Dinchuk,J.E., Burn,T.C., Hollis,G.F. and
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Henderson,N.L., Dinchuk,J.E., Burn,T.C., Hollis,G.F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.5%; Score 35; DB 10; Length 4419; Best Local Similarity 100.0%; Pred. No. 7.3e-07; Matches 35; Conservative 0; Mismatches 0; Indels (
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20564328
10956665
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AF289215.2 GI:13310928
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musculus (house mouse)
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Direct Submission
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AUTHORS
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/produCt-"aspartyl beta-hydroxylase 6.6 kb transcript"
/db xref="d1:11878112"
/db xref="d1:11878112"
/db xref="d1:11878112"
/db xref="d1:11878112"
/db xref="d1:1187812"
/db
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Mouse DNA sequence from clone RP23-152A20 on chromosome 4, complete
Dinchuk, J.E., Henderson, N.L., Burn, T.C., Huber, R., Ho, S.P.,
Link, J., O'Neil, K.T., Focht, R.J., Scully, M.S., Hollis, J.M.,
Hollis, G.F. and Friedman, P.A.
Aspartyl beta - hydroxylase (Asph) and an evolutionarily conserved
isoform of Asph missing the catalytic domain share exons with
                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (26-7UL-2000) Applied Biotechnology, DuPont
Pharmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400, USA
Location/Qualifiers
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                                                                                                                                                                              Biol. Chem. 275 (50), 39543-39554 (2000)
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. 7.3e-07;
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/chromosome="8"
/map="8q12 at STS WT-11767"
/tissue_type="liver"
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llarity 100.0%; Pred. No. 7.3
Conservative 0; Mismatches
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strain="BALB/c"
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AL671970.8 GI:46878903
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/gene="Asph"
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/gene="Asph"
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'gene="Asph"
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mkna linear ROD 18-DEC-2000 mena musculus aspartyl beta-hydroxylase cardiac isoform 1 (Asph) mena, partial cds; alternatively spliced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sangcr.ac.uk/Projects/C elegans/wormpep This sequence http://www.sangcr.ac.uk/Projects/C elegans/wormpep This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

RP23-152A20 is from the RPCI-23 Mouse BAC Library
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

Location/Qualifiers
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                               Chordata, Craniata, Vertebrata, Buteleostomi,
Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                         Submitted (29-APR-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 29, 2004 this sequence version replaced gi:21531211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73512 TCTTTCCGGCTGATATTCATCGTGGATGTGTGGCA 73478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2208 TCTTTCCGGCTGATATTCATCGTGGATGTGTGCCA 2242
                                                                                                                                                                                                                                                                                                                                                                     Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/clone_lib="RPCI-23"
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Mus musculus (house mouse)
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Mus musculus
Eukaryota; Metazoa; Cho:
Mammalia; Eutheria; Rodi
1 (bases 1 to 168569)
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Carminci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramaon, R.D., Mullahy, S.J., Bosak, S.A., McSwan, P.J., Peters, G.J., McSwan, P.J., Mullahy, S.J., Malek, J.A., Gunaratne, P.H., Richards, S. Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Mushy, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodriques, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Sheychenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Snailus, D.E., Schmerch, A., Schsi, Krzywinski, M.I., Skalska, M. Sanilus, D.E., Schnerch, A., Schsi, J. S., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

E. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   // Anches—Aspa B-Hydro, N. Region: Aspartyl beta-hydroxylase N-terminal regions. This family includes the N-terminal regions of the junctin, junctate and aspartyl beta-hydroxylase proteins. Junctate is an integral BK/SR membrane calcium binding protein, which comes from an alternatively spliced form of the same gene that generates aspartyl beta-hydroxylase and junctin. Aspartyl beta-hydroxylase the post-translational hydroxylation of aspartic acid or asparagine residues contained within epidermal growth factor (EGF) domains of proteins.
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/product=="Unknown" (protein for MGC:74216)"
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/db_xref="G1:817949"
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ISEVLYGHKNGRRGGISGSSFTWFWYIALLGUTKNGSNEWIDSLEEVLITLAEBSSDWF
YGFLSFLYDIMTPFEMLEBEBEBESETADGVDGKTCVILDLHNQ"
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through the I.M.A.G.B. Consortium/LLML at: http://image.llnl.gov
Sexies: IRAL plate: 53 Row: a Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 12746447.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg, R. Strausberg, R. Direct Submission National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: MGC help desk First Contact: MGC help desk Email: Ggapbe-r@mail.nih.gov Tissue Procurement: Dr. Michael Brownstein CDNA Library Preparation: Michael Brownstein / Ted Usdin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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/db xref="taxon:10090"
/clone="MGC:74216 IMAGE:6533192"
/tissue type="Brain, mouse"
/clone lib="NHH MGC_144"
/lab_nest="bH10B"
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COMMENT
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WPDLVDEWLGAGKGYVDADGGOSDFDVDDAKVLLGUKERSPSERTFPPERAETHAELEE
QAPEGADIQNVEDEVKEQIQSLLQESVHTDH"
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BC061098.1 GI:38173948
MGC.
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1763)
Straubberg,R.L., Feingold,B.A., Grouse,D.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altechul,S.F., Zeeberg,B., Buetow,K.H., Scheefer,C.F., Bhat,N.K.,
Hopkins,R.P., Jordan,H., Moore,T., Max.S.I., Wang,J., Heideh,F.,
Stapleton,M., Soarees,M.B., Benaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammallai, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Musi (Dases 1 to 524)
Dinchuk, J. E., Henderson, N. L., Burn, T. C., Huber, R., Ho, S. P., Link, J., O'Nell, K. T., Pocht, R. J., Scully, M. S., Hollis, J. M., Hollis, G. P. and Priedan, P. D. Aspartyl beta hydroxylase (Asph) and an evolutionarily conserved
                                                                                                                                                                                                                                                                      Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125. .>524
/gene="Asph"
pplice="asparaginyl beta-hydroxylase; AspH; alternatively
spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (25-JUL-2000) Applied Biotechnology, DuPont
Pharmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400, USA
Location/Qualifiers
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Dinchuk, J.E., Henderson, N.L., Burn, T.C., Hollis, G.F. and
Friedman, P.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
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1. .>524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="Asph"
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BC061098
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LOCUS DEFINITION

ACCESSION VERSION

KEYWORDS

SEGMENT

SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

RESULT 41 H010058S02

Matches

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ORIGIN

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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. C. 1 (bases 1 to 2770)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Schenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheefer, C.F., Bhat, N.K., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheefer, T.B., Brands, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Worley, K.C., Hale, S., Garciare, P.H., Richards, S., Worley, K.C., Hale, S., Garciar, M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, F.J., Lu, X., Gibbs, R.A., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Komman, J.W., Schein, J.B., Schein, J.B., Jones, S.J. and Marra, M.A., Aman, J. A., Jones, S.J. and Marra, M.A., A., A., A., A., M. and Marra, M.D., Romener, A., M. and Marra, M.D., Schein, J.B., Jones, S.J. and Marra, M.A., Schein, J. B., Jones, S.J. and Marra, M. B., J. A., J. 
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FEDLEBGTVHEBIBOTYHVEDTASQNHPNDMEEMTNEQENSDPSEAVTDAGVLLPHAE
EVRHODYDEPVYEPSEHEGVEISDNTIDDSSIISEEINVASVEEQQDTPPDT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tränslation="naedkeakhgghkngrrggisggsftwfmviallgvwtsvavv
wfdlvdyeevlgklgvydadgdgdfdvddakvllglkerspsertfefeaethaelee
                             2 (bases I to 2617)
Hong.C.-S. and Kim.D.H.
Direct Submission
Submitted (05-SEP-2000) Life Science, Kwangju Institute of Science
and Technology, Puk.gu, Oryong-dong, Kwangju 500-712, South Korea
on Oct 29, 2001 this sequence version replaced gi:15824389.
Location/Qualifiers
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.4%; Score 32; DB 10; 1
100.0%; Pred. No. 3.3e-05;
tive 0; Mismatches 0;
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/protein id="AAL09319.2"
/db_xref="GI:16507231"
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                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
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BC015281.1 GI:15929715
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Best Local Similarity 100.0
Matches 32; Conservative
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Direct Submission
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Unpublished
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Mus musculus aspartyl beta-hydroxylase (ASPH) gene, exon 3.
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Dinchuk, J. E., Henderson, N. L., Burn, T. C., Huber, R., Ho, S. P., Link, J., O'Neil, K. T., Focht, R. J., Scully, M. S., Hollis, J. M., Hollis, G.F. and Friedman, P. A.
Aspareyl beta hydroxylaee (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
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Sciurognathi, Muridae, Murinae, Mus
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Submitted (25-JUL-2000) Applied Biotechnology, DuPont
Submitted (25-JUL-2000) Applied Biotechnology, DuPont
Pharmaceuticals Company, PO BOX 80400, Wilmington, DE 19880, USA
Location/Qualifiers
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Henderson, N.L., Dinchuk, J.E., Burn, T.C., Hollis, G.F. and
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Mus musculus cardiac junctate 1 mRNA, complete cds
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100.0%; Pred. No. 3.2e-05;
tive 0; Mismatches 0;
                                                                                               Score 32; DB 10; I
Pred. No. 3.2e-05;
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100.0%; Pred. No. ...
0; Mismatches
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Acganism="Mus musculus"
mol type="genomic DNA"
db xref="taxon:10090"
1105. .1173
/gene="ASPH"
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Mammalia; Eutheria; Rodentia; Sciu
I (bases 1 to 2617)
Hong, C.-S. and Kim, D.H.
Cloning of mouse junctin homologs
                 /db_xref="CDD:pfam05279"
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Mus musculus
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Mus musculus (house mouse)
Mus musculus
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RESULT 42 AF302653

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Mouse DNA sequence from clone RP23-70D2 on chromosome 4, complete
            Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 2789)
Dinchuk,J.E., Henderson,N.L., Burn,T.C., Huber,R., Ho,S.P.,
Link,J., O'Neil,K.T., Focht,R.J., Scully,M.S., Hollis,J.M.,
Hollis,G.P. and Friedman,P.A.
Aspartyl beta -hydroxylase (hsph) and an evolutionarily conserved
isologom of Asph missing the catalytic domain share exons with
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Dinchuk,J.E., Henderson,N.L., Burn,T.C., Hollis,G.F. and
Friedman,P.A.
Direct Submission
Submitted (26-JUL-2000) Applied Biotechnology, DuPont
Pharmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400, USA
1. 2789
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/gene="Asph"

/note="Humbug; asparaginyl beta-hydroxylase; AspH;

/note="Humbug; asparaginyl beta-hydroxylase; AspH;

non-catalytic isoform; alternatively spliced"
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J. Biol. Chem. 275 (50), 39543-39554 (2000)
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/gene="Asph"
2783. .2788
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                                                                               WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Diff Technologies, Inc.
CDNA Library Preparation: Diff Technologies, Inc.
CONDA Library Preparation: Diff Technologies, Inc.
CONDA Library Preparation: Diff Technologies, Inc.
CONDA Library Preparation: Diff Technologies, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
CONDACT: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRMK Plate: 25 Row: e Column: 8
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 12746447
This clone has the following problem: The cds is short compared to the longest cds in the locus.

Location/Qualifiers
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/product="Asph protein"
/product="Asph protein"
/brotein id="AAH15281.1"
/db_xref="Gi.15929716"
/db_xref="MGI.1914186"
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/tb_xref="MGI.1914186"
/tb_xref="MGI.NGREGSFFTWRMVIALLGWWTSYAVWPDLVDYEBVLGKLGVVDAD
GDGPPDVDDAVVLLGLKERSPERFTFPPEAETHAELBEQAPEGADIGWTBDRYGDL
GDGSVATPUHDEADGLAGEPQPEVEDFLTVTDSDDRFEDLEFGTVHEETEDTYPHVB
DTASQNATPHDMEEADGLAGEPQPEVEDFLTVTDSDDRFEDLEFGTVHEETEDTYPHVB
DTASQNATPROMBEMTINEQENSEEVRHQDYDEPVYEPSEHEGVEISDNTIDDSSIISEE
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Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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db_xref="LocusID:65973"

db_xref="WGI:1914186"
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gene="Asph"
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/gene="Asph"
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/map="8q12 at STS WT-11767"
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                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
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                                                                                                                                                                                                                                                                                                           db_xref="taxon:10090"/chromosome="8"
                                                                                                                                                                                                                                                                                                                                                                         'tissue_type="heart"
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AF221854.1 GI:12655824
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Best Local Similarity
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                                                                                                                       Friedman, P.A.
                 J. Biol.
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                                                                                                                                                                                                                                                                                       During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 566)
Dinchuk, J.E., Henderson, N.L., Burn, T.C., Huber, R., Ho, S.P.,
Dinchuk, J.E., Henderson, N.L., Scully, M.S., Hollis, J.M.,
Hollis, G.F. and Friedman, P.A.
Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-70D2 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                        Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/clone_lib="RPCI-23"
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Location/Qualifiers
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KEYWORDS
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                               REFERENCE
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Butaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Butaryota, Muteria; Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 919)
Jones, L.R., Zhang, L., Sanborn, K., Jorgensen, A.O. and Kelley, J. Jones, L.R., Zhang, L., Structure, and immunological characterization of the 26-kDa calsequestrin binding protein (junctin) from cardiac junctional sarcoplesmic reticulum 96 (1995)
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/product="asparty1 beta-hydroxylase cardiac isoform 2"
/protein_id="AAG40814.1"
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/db_xref="cd::11878122"
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/tb_xref="cd::11878122"
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/tb_xref="cd::11878122"
/tb_xref="cd::11878122"
/tb_xref="cd::1187812"
/tb_xref="cd::11
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Direct Submission
Submitted (06-JAN-2000) 47, Sigma Chemical Co., N-3, 3300 South
                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (26-UUL-2000) Applied Biotechnology, DuPont Pharmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400, USA Location/Qualifiers
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                                                                                                                                                                                             2 (bases 1 to 566)
Dinchuk, J.E., Henderson, N.L., Burn, T.C., Hollis, G.F. and
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143. .766
/note="calsequestrin binding protein"
Chem. 275 (50), 39543-39554 (2000)
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100.0%; Pred. No. 0.00011;
tive 0; Mismatches 0;
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Location/Qualifiers
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/procein_id="AANB7549.1"
/db_xref="G1:27261146"
/db_xref="G1:2726114
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Direct Submission
Submitted (12-JAN-2000) Life Science, Kwangju Institute of Science and Technology (K-JIST), Puk-gu, Oryong-dong, Kwangju 500-712,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROD 18-DEC-2000
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (Dases I to 1013)
Hong, C. and Kim, D.H.
Mouse junctin-1 mRNA
Unpublished
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Dinchuk, J. E., Henderson, N. L., Burn, T. C., Huber, R., Ho, S. P., Link, J., O'Neil, K. T., Focht, R. J., Scully, M. S., Hollis, J. M., Hollis, G. F. and Friedman, P. A.
Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
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Submitted (26-JUL-2000) Applied Biotechnology, DuPont
Pharmaceuticals, D. O. Box 80400, Wilmington, DE 19880-0400, USA
Location/Qualifiers
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Dinchuk, J.E., Henderson, N. L., Burn, T.C., Hollis, G.F. and
Friedman, P.A.
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//crganiam="Mus musculus"
/mol type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/tissue type="heart"
168 .791
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/product="junctin-1"
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19, C. and Kim, D.H.
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/codon_start=1
/product="cardiac junctin"
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GEDRGKGKKKPDSDTSOKASAAGKRDBDKEKASSDKSSKSKESWKKAVETKAVSSKVA
ARDKDRRGRSSGGHAHVSKENGQKRKN"
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1.3%; Score 31; DB 10; Length 988;
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/organism="Mus musculus"
/organism="Mus musculus"
/mol type="mmsn"
/strain="maxlsn"
/db xref="taxon:10090"
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/protein_id="AAN87550.1"
/db_xref="G1:27261148"
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*** SEQUENCING IN PROGRESS ***.
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1 (bases 1 to 158289)
Csuros,M. and Milosavljevic,A.
Pooled genomic indexing (PGI): mathematical analysis and experiment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Springer (2002)
2 (bases 1 to 158289)
Milosavljevic, A., Sodergren, E., Csuros, M., Li, B., Jackson, A.R.,
Adams, C., Adio-Oduola, B., All-osman, F.R., Allen, C., Alsbrooks, S.L.,
                                                                                                     ROD 29-OCT-2001
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Hong, C.-S. and Kim, D.H.

Hong, C.-S. and Kim, D.H.

Direct Submitssion

Submitted (05-SEP-2000) Life Science, Kwangju Institute of Science and Technology, Puk-gu, Oryong-dong, Kwangju 500-712, South Korea Location/Qualifiers
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 2637)
Hong, C.-S. and Kim, D.H.
Cloning of mouse junctin homologs
Unpublished
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(in) Guigo,R. and Gusfield,D. (Eds.);
ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI
2002, ROME, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS: 10-28;
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Mus musculus cardiac junctate 2 mRNA, complete cds.
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/protein_id="AAL09320.1"
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120. 899
                                                                                                                                                                                                                    Mus musculus (house mouse)
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Unpublished
(bases 1 to 2432)
Hong,C.-S. and Kim,D.H.
Direct Submission
Submitted (05-SEP-2000) Life Science, Kwangju Institute of Science Submitted (05-SEP-2000) Life Science Submitted (05-SEP-2000)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bass 1 to 2432)

Hong, C.-S. and Kim, D.H.

Cloning of mouse junctin homologs
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1.3%; Score 31; DB 10; Length 2432;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 31; Conservative 0; Mismatches 0; Indels
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Mus musculus cardiac junctate 3 mRNA, complete cds.
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Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 31; Conservative 0; Mismatches 0;
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Manaratunga, H.C., Arte, J. R., Ayete, N., Banks, T., Barbarla, J., Bankarga, M., Brown, B., Burgaga, M., Brown, B., Brown, M., Brown, B., Brangag, M., Brown, B., Brown, M., Brown, D., Bouck, J., Burcel, P., Burket, C., Briewa, M., Brown, B., Brown, M., Bryant, N. P., Buhay, C., Burch, P., Burket, C., Carron, T. F., Chiu, D., Chowdhry, J., Chistopoulos, C., Clarcon, T. F., Cox, C., Coyle, M.D., Chowdhry, J., Chistopoulos, C., Clarcon, T. F., Davy, Carroll, L., Didgard, D., David, R., Davida, M.L., Davis, C., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K. J., Darger, H., Bury, Carroll, L., Ding, Y., Dubin, H.H., Douthwaite, K. J., Darger, H., Ellaj, C., Emerling, S., Escotto, M., Faris, P., Ferraguto, D., Flagga, N., Ford, J., Foren, M., Gill, R., Gorrell, J. H., Guevara, W., Gunazatne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hant, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, C., Harris, K., Howard, S., Huber, J., Holloway, C., Hollins, B., Homai, P., Jawes, M., Hullyk, S., Hume, J., 108hkhes, I., Jackson, L.E., Jacobson, B., Jiat, Y., Johnson, R., Ollins, B., Homai, P., Karlovic, J., Kratovic, J., Kratovic, J., Kratovic, J., Kratovic, J., Kratovic, J., Lid, Y., Johnson, R., Man, J., Martindale, M., Martin, Mapue, P., Marcier, R., Marcier, M., Martindale, M., Martin, Mapue, P., Marcier, R., Martindale, M., Martin, Mapue, P., Marcier, R., Martindale, M., Martin, M., Mayoen, W., Nickerson, E., Neben, J., Martindale, M., Mell, M., Martin, M., Mayoen, N., Nickerson, E., Neben, M., Nickerson, E., Marten, M., Mayoen, N., Nighen, M., Marten, R., Marten, R., Marten, R., Marten, R., Marting, M., Marting, M., Marting, M., Marting, M., Marten, R., Staney, C., Scherer, S., Scott, G., Shen, H., Stone, H., Stone, H., Stone, H., Stone, H., Walliamson, Marting, M., Washington, C., Watlington, S., Walliamson, M., Warten, R., Washington, C., Watlington, S., Walliamson, M., Walliamson, M., Washington, C., Watlington, S., Walliamson, M., Walliamson, M., Walliamson, M., Walliamson, M., Walliamson, M., 
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* (See http://www.hggc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: The contigs are based on the application

* of the PGI method using the Human genome (NCBI build 31)

* as the Comparative genome.

* NOTE: This is a 'working daraft' sequence. It currently

* consists of I contigs. Gaps between the contigs

* are represented as tuns of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: http://www.hgsc.bcm.tmc.edu/
Contact: http://www.hgsc.bcm.tmc.edu/
Center project Information
Center project Information
Center project Information
Center clone name: LR50-269N19
Center clone name: CR50-269N19
Center Lone name: CR50-269N19
Consensus quality: 7790 bases at least Q10
Consensus quality: 10542 bases at least Q20
Consensus quality: 10542 bases at least Q20
Amaratunge, H.C., Are, J.R.,
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AUTHORS
TITLE
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COMMENT

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Ratues.

I (bases I to 234548)

Miller, A. Melzher, Merzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Anjen, C., Allen, H., Alsbrocks, S., Amin, A., Anginano, D., Anjen, C., Allen, H., Alsbrocks, S., Amin, A., Anginano, D., Anjen, C., Alsbrocks, S., Amin, A., Magailano, D., Bandaranike, D., Barder, M., Barastead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Brwalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Charez, D., Chen, G., Chen, R., Chen, Y., Charez, D., Chen, G., Chen, R., Chen, Y., Chares, D., Chanson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Davis, S., Denson, S., Denson, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Ermandez, S., Finley, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Farnandez, S., Finley, M., Hangy, M., Gorrer, W., Gebrer, C., Gabis, A., Ganter, T., Garra, M., Gebregeorgis, E., Geer, K., Glill, R., Garder, M., Gerra, W., Gebrer, C., Madbis, A., Handin, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, M., Harnandez, J., Harnandez, J., Havlak, P., Hawes, A., Honderson, N., Hogues, M., Harnandez, M., Harnandez, M., Harnandez, J., Hawes, A., Johnson, R., Marpathy, S., Kelly, S., K
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Rattus norvegicus clone CH230-8Kl, WORKING DRAFT SEQUENCE, 2
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* the accession number will be preserved.

* Location/Qualifiers

1. 158289

/organism='Macaca mulatta"

/ do _type='genomic DNA"

/ do _type='genomic DNA"

/ do _type='genomic DNA"

/ do _tope='genomic DNA"

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HTG; HTGS PHASB1; HTGS_DRAFT; HTGS_FULLTOP.
RATTUS NOTVEGICUS (NOTWAY rAL)
RATTUS NOTVEGICUS
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AC095635/c
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DEFINITION
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Worley, K.C.

Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department Submitted (17-SEP-2001) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Skat Genome Sequencing Consortium.

Direct Submission

Submitted (09-MAY-2003) Human Genome Sequencing Center, Department Submitted (09-MAY-2003) Human Genome Sequencing Center, Department Of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:24817791.

The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.Dgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence cases. Both end sequences and whole genome table.
Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Railly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Slsson, I., Sitter, C.D., Smajs, D., Sreimed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tablor, P., Taylor, C., Taylor, T., Thomas, M., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, C., Wang, S., Warren, R., Weizk, M., While, F., Wilson, R., Walson, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Vu, F., Zhang, J., Zhou, J., Zhou, Y., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R.A., Smith, H.O., Hand, H.D., Hand, H.D.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 222438 bases at least Q40 consensus quality: 224642 bases at least Q30 consensus quality: 225972 bases at least Q30 sessing that ity: 225972 bases at least Q20 Estimated insert size: 232080; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
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232994

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FEATURES

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Rattus.

In (bases 1 to 275547)

Rattus.

Rattus.

Merzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,

Allen, H., Alpacia, A., Anguiano, D.,

Allen, H., Alpacoks, S., Amin, A., Anguiano, D.,

Anyalebechi, V., Avagia, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranik, D., Barber, B., Burber, P., Brown, H.,

Biswalo, K., Blair, J., Blaire, P., Burrell, K., Calderon, E.,

Cracenso, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z.,

Cracenso, J., Chavez, D., Chen, G., Chen, R., Chen, R., Chen, R.,

Cracenso, J., Chavez, D., Chen, G., Chen, R., Chen, R., Debard, C., Dever, J.,

Cracenson, S., Deramo, C., Dany-Carroll, L., De Anda, C., Dederich, D.,

Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Dayla, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Daper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B.,

Egan, A., Bscotto, M., Enger, C., Evans, C.A., Garner, T., Garza, M.,

France, C.M., Gabisi, M., Hamil, C., Hamilton, C., Hamilton, K.,

Gebregergis, E., Geer, K., Gill, R., Grady, M., Hernandez, J.,

Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M.,

Holling, B., Howells, S., Hulyk, S., Hume, J., Idebird, D., Jackson, A.,

Jackson, L., Jacob, L., Lebow, H., Levan, J., Ledris, L., Kovar, C.,

Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,

Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,

Lorensuhewa, L., Loulseged, H., Loadson, J., Maller, M., Marlin, R.,

Mannshwar, M., Liu, Y., London, P., Longacre, S., Mad, J.,

Mannshwar, M., Liu, Y., London, P., Longacre, S., Pan, M., Murphy, M., Martin, K., Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus clone CH230-16022, WORKING DRAFT SEQUENCE, 4 unordered pieces.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                              Gaps
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0
                                                                                                                                                                                                                                        Length 234548;
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      175547 GGTCTCTTCCTGCCTGAGGATGAAAACCT 175519
organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                             1839 GGTCTCTTCCTGCCTGAGGATGAAACCT 1867
                                                                                                                                                                                                                                            Query Match
1.2%; Score 29; DB 3
Best Local Similarity 100.0%; Pred. No. 0.00
Matches 29; Conservative 0; Mismatches
                             /mol_type="genomic DNA"
/db xref="taxon:10116"
                                                        /db_xref="taxou...
/clone="CH230-8K1"
                                                                                                                          1. .1711
/note="wgs_contig"
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                                                                                                                                 misc_feature
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DEFINITION
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PAT 27-SEP-2004

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COMMENT

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H010058805 2013 bp DNA linear ROD 13-MAR-2001 Mus musculus aspartyl beta-hydroxylase (ASPH) gene, exon 15. AF289209.1 GI:11692638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murphy, F.J., Sheehan, D.E., Keating, K.E., Hayes, I.E. and Seera, L.E. Enzymes involved in apoptosis
Patent: WO 2004078783-A 156 16-SEP-2004;
Eirx Therapeutics Lid (IE)
Location/Qualifiers
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
(Dases 1 to 2013)
Dinchuk, J.E., Henderson, N.L., Burn, T.C., Huber, R., Ho.S.P.,
Link, J., O'Neil, K.T., Focht, R.J., Scully, M.S., Hollis, J.M.,
Hollis, G.P. and Friedman, P.A.
Rapartyl beta -hydroxylase (Asph) and an evolutionarily conserved
isoform of Asph missing the catalytic domain share exons with
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Henderson, N.L., Dinchuk, J.E., Burn, T.C., Hollis, G.F. and
                                                                                                                                                                                                                                                                                             1.2%; Score 29; DB 2; Length 275547;
100.0%; Pred. No. 0.0015;
tive 0; Mismatches 0; Indels 0;
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20564328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="synthetic construct"
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/noTe="QPCR primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CQ871665 27 bp DNA Sequence 156 from Patent WO2004078783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    28866 GGTCTCTTCCTGCCTGAGGATGAAAACCT 28838
                                                                                                                                                                                                                                                                                                                                                                                                                 1839 GGTCTTCCTGCCTGAGGATGAAACCT 1867
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26655. .267994
/note="wgs contig"
/oots. .269305
                                                                                                                                                                  268045. .269305
/note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CQ871665.1 GI:52745698
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CQ871665/c
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Contact: hgsc-help@bcm.tmc.edu

Center project Information
Center project Information
Center project name: KAFS
Center clone name: KAFS
Center clone name: CH230-16622
Assembly program: Phrap; version 0.990329
Consensus quality: 223348 bases at least Q40
Consensus quality: 225882 bases at least Q40
Consensus quality: 225881 bases at least Q20
Consensus quality: 225881 bases at least Q20
Consensus quality: 227831 bases at least Q20
Estimated insert size: 224883; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, Y., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., Von, Weinsern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 269305: contig of 269305 bp in length 269405: gap of unknown length 273198: contig of 3693 bp in length 273198: gap of unknown length 274358: contig of 1160 bp in length 275547: contig of 1089 bp in length 10ccation/Qualifiers
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Center: Baylor College of Medicine
Center code: BCM
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                                                                                                                                                                                                                                                                                                2 (bases 1 to 275547)
Worley, K.C.
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FEATURES

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Gaps

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Nuzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allan, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi V., Aoyagi, A., Aydegi, M., Baca, E., Baden, H., Bandlebchi V., Aoyagi, A., Aydegi, M., Baca, E., Baden, H., Bandlebchi V., Bardarbo, Barber, M., Barber, M., Bandranaike, D., Barber, M., Barber, M., Bandra, M., Bandra, M., Bhay, C., Burch, P., Burchl, K., Calderon, E., Cadena, V., Chen, G., Chen, G., Chen, G., Chen, R., Chen, Y., Chen, T., Chen, Y., Chen, T., Chen, Y., Chen, T., Chen, G., Chen, G., Chen, R., Chen, Y., Chen, T., Chen, G., Davaia, M. Davila, M.L., Davais, C., Darano, C., Durol, C., Deferich, D., Denson, S., Deramo, C., Durol, M., Cree, A., D'Souza, L., Delgado, O., Denson, S., Deramo, C., Bardo, Y., Dih, H., Divya, K., Egan, A., Escotto, M., Bageer, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flager, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flager, M., Ganta, R., Garre, M., Gebregoorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, M., Guevara, M., Harnandez, M., Havlak, P., Hadand, M., Hamilton, K., Harlak, P., Hadand, M., Hamilton, K., Harlak, M., Handerson, N., Hernandez, J., Howells, S., Hulk, M., Homerson, N., Hernandez, J., Jackson, L., Jacob, L., Jang, H., Johnson, B., Johnson, R., Johnson, R., Johnson, R., Johnson, L., Jacob, L., Jang, H., Lorado, R., Johnson, E., Lui, Y., Liu, W., Liu, Y., Karlak, C., Liu, G., Kraft, C., L., Lebow, H., Lorado, R., Johnson, B., Johnson, B., Mandewari, M., Mahindey, S., Marchin, S., Marlin, S., Marlin, R., Martin, R., Martinez, E., Manderylevic, A., Martin, M., Perez, M., Perez, M., Perez, M., Perez, M., Perez, M., Perez, M., Perez,
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252366 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-11D6, WORKING DRAFT SEQUENCE, 3
unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                      Direct Submission
Submitted (25-JUL-2000) Applied Biotechnology, DuPont
Pharmaceuticals Company, PO BOX 80400, Wilmington, DE 19880, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.2%; Score 27; DB 10; Length 2013;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 27; Conservative 0; Mismatches 0; Indels (
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AC096178.6 GI:30522511
HTG; HTGS, PHASE1; HTGS, DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                            1. 2013

'Organism="Mus musculus"

/mol type="genomic DNA"

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/gene="A&FH"

/number=15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1077 AAAATTGAGGAAGCAGTGAATGCATTT 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 AAAATTGAGGAAGCAGTGAATGCATTT 321
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Friedman, P.A
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AC096178
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AL Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Daylor Plaza, Houston, TX 77030, USA
Daylor Plaza, Houston, TX 77030, USA
Daylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:24818276
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both be indicated in the feature table.
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scheret, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soaa, J., Steimle, M., Strong, R., Sutton, A., Vatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldren, B., Wang, J., Walter, F., Wallson, R., Warzen, R., Woden, H., Worley, K., Willson, R., Wals, S., Yen, J., Yoon, U., Yoon, U., Yoon, U., Yoon, J., Zhou, A., Zhou, S., Dunn, D., von Niederhausern, A., Waiss, R., Smith, D.R., Holt, R.A., Smith, D.R., Walts, S., Smith, D.R., Holt, R.A., Smith, D.R., Walts, S., Submission
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Center: Cade: BCM
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project name: GEPB
Center clone name: CH230-11D6
Center clone name: CH230-11D6
Center graphy program: Atlas 3 0;
Consensus quality: 233032 bases at least Q40
Consensus quality: 233946 bases at least Q20
Consensus quality: 235460 bases; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley,K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department Submitted (17-SEP-2001) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (Dases 1 to 252366)
Rat Genome Sequencing Consortium.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 248556: contig of 248556 bp in length
57 248656: gap of unknown length
57 250663: contig of 2007 bp in length
64 250763: gap of unknown length
64 252366: contig of 1603 bp in length.
Location/Qualifiers
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Direct Submission

L Submission

Submission

Pharmaceuticals Company, PO BOX 80400, Wilmington, DE 19880, USA

Location/Qualifiers

I. 1209e.

forganism="Mus musculus"

Anol type="genomic DNA"

Ab zref="taxon:10090"

Ngone="ASPH"

/mumber=22

n /gene="ASPH"

/mumber=23
                                                                                                         H010058810 12095 bp DNA linear ROD 13-MAR-2001 with musculus aspartyl beta-hydroxylase (ASPH) gene, exons 22 and
                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Butheria, Rodentia, Sciurognathi; Muridae, Murinae; Mus. 1 (bases 1 to 12095)
Dinchuk, J. E., Henderson, N. L., Burn, T. C., Huber, R., Ho, S. P., Link, J. O'Neil, K. T., Focht, R. J., Scully, M. S., Hollis, J. M., Hollis, G. P. and Friedman, P. A.
Rapartyl beta -hydroxylase (Asph) and an evolutionarily conserved isocome of Asph missing the catalytic domain share exons with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF016503
AF016503
AF016503.1 GI:4102918
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Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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1 (bases 1 to 1519)
Masuda,M., Igarashi,H., Kano,M. and Yoshikura,H.
Proviral Integration into the Procollagen C-proteinase Enhancer
Protein Gene and Its Effects in Cultured Rat Fibroblasts Revealed
by an Excisable 'Hit-and-Run' Retroviral Vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 12095)
Henderson, N. L., Dinchuk, J. E., Burn, T. C., Hollis, G. F. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 275 (50), 39543-39554 (2000)
20564328
        1809 GGCTTCATCCTGAAGGCACAGAACAA 1834
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                                                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                   AF289214
AF289214.1 GI:11692643
                                                                                                                                                                                                                           10 of 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10956665
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KEYWORDS
SEGMENT
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                                                                 RESULT 60
H010058S10
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AF016503/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H010058807 6629 bp DNA linear ROD 13-MAR-2001
Mus musculus aspartyl beta-hydroxylase (ASPH) gene, exons 18 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dinchuk,J.E., Henderson, N.L., Burn,T.C., Huber,R., Ho,S.P.,
Link,J., O'Neil,K.T., Focht,R.J., Scully,M.S., Hollis,J.M.,
Hollis,G.F. and Friedman,P.A.
Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved iseform of Asph missing the catalytic domain share exons with
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Submitted (25-JUL-2000) Applied Biotechnology, DuPont
Pharmaceuticals Company, PO BOX 80400, Wilmington, DE 19880, USA
Location/Qualifiers
1. 6629
| /organism="Mus musculus"
| mol type="genomic DNA"
| db_xref="learon:10090"
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Henderson, N.L., Dinchuk, J.E., Burn, T.C., Hollis, G.F. and
Priedman, P.A.
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1.2%; Score 27; DB 2; Length 252366;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 27; Conservative 0; Mismatches 0; Indels 0
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20564328
organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                 170125 AAAAGAACAAATTCAGTCCCTTCTCCA 170151
               /mol_type="genomic_DNA"]
/db_xerE="taxon:10116"
/clone="fH230-11D6"
264. :906
/note=="clone_boundary
clone_end:T7
site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                           452 AAAAGAACAAATTCAGTCCCTTCTCCA 478
                                                                                                                                                                          20540. 40522
/note="Clone boundary
clone_end:Sp6
site:ECORI
end_sequence:BH340112"
                                                                                                                                                    end_sequence:BH340110"
20540. .40522
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AF289211.1 GI:11692640
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4834. .4923
/gene="ASPH"
/number=19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1764. .1862
/gene="ASPH"
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                                                                          misc_feature
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H010058S07
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1494 GGCTTCATCCTGAAGGCACAGAACAA 1519

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/codon_start=1
                                                                                         'gene="txk"
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Best Local Similarity 100.
Matches 24; Conservative
                                                                                                              84. .1667
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MMU16145/c
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                                                                                                                                                                                                                                                                                                                                                                                              /translation="MLPAALTSLLGPFLLAMVLPLARGOTPNYTRPVFLCGGDVTGES
GYVASBGFPNLVPPNKKCI WITTVPEGGTVSLSFRVPDMELHPSCRYDALEVFAGSGT
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RMFFAGGTLTPNWPESDYPGISCSWHIIAPSNGVIMLFFGKFVDFDDTYCRYDSVS
RMFFAGGTLTTPNWPESDYPGISCSWHIIAPSNGVIMLFFGKFVDFDDTYCRYDSVS
VEKESABSPGEDAQHGPGSRSDFRTGTGFKVRVSDESVYTADGFSASYRTLFRDA
VBREAASPGEDAQHGPGSRSDFRTGTGFKVKAWRGGGEGLTTVYSLLGVYKTGDL
DLBSPAGTTSLKFYVPCKQMPPWKKGASYLLMQQVEBNRGFILDPFSFVVLYRPNQDQ
ILSNLSKRKCPSQPRPDA"
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             Masuda, M. and Igarashi, H.
Direct Submission
Submitted (30-JUL-1997) Department of Microbiology, Graduate School
of Medicine, The University of Tokyo, 7-3-1 Hongo, Bunkyo-ku, Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1680)
Sommers, C.L., Huang, K., Shores, E.W., Grinberg, A., Charlick, D.A., Mozak, C.A., and Love, P.E.
Murine txk: a protein tyrosine kinase gene regulated by T cell activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (09-JAN-1995) Connie L. Sommers, National Institute of Child Health and Human Development, National Institutes of Health, Bldg. 6B, Rm. 28210, Betheeda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                         product="procollagen C-proteinase enhancer protein"
protein id="AAD01592.1"
db_xref="GI:4102819"
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Mus musculus tyrosine kinase TXK (txk) mRNA, complete cds.
U19607
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                                                                                                                       1. .1519

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/mol_type="mRNA"

/strain="r344"

/db xref="taxon:10116"

/cell_line="Rat2"

/cell_type="fibroblast"

/dev_stage="embryo"

1. .1519
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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95349947
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                                                                                                      Location/Qualifiers
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Mus musculus
                                                                                                                                                                                                                                                                                   'gene="PCPE"
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(bases 1 to 1519)
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                                                                                           113, Japan
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 220%) Haire, R.N. and Litman, G.W. The murine form of TXK, a novel TEC kinase expressed in thymus maps to chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERLLRQEAKEGAFI VRDSRHLGSYTI SVFTEARRHTOSSI KHYOIKKNDSGOWYTTER
HLFPSVPELLOYHOYNAAGLI SRLRYPI GLLGSCLPATSGFSYEKWEI DPSELAFVKE
I GSGOFGVVHLGEWRAHI PVAI KA INBGSNSEEDFI EBAKVMMKLGHSRAVOLYGVCI
OOKDLY YVTERWROGCLDYIJERKGOLQKALLLLSWCODI CEGMAYLERSCY IHRDLA
ARNCLVSSACVYKI SDFGMARYVLDDEYISSSGAKFPVKWCPPBVFHFNKYSSKSDVM
SFGVLMMRVFTBGRANFENKSNLQVVBAI SQGFRLYRPHLAPMTI YRVMYSCWHESPK
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/db_xref="G1:643065"
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LKRAEEYLILERCDPHWWKARDRFGNEGILDSNYVTENRLANLEIYEWYHKNITRNQT
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Direct Submission

Submitted (19-OCT-1994) Gary W. Litman, Molecular Genetics, All

Children's Hospital, 801 6th Street S., St. Petersburg, FL 33701,

USA
                                                                                                                                                                                                                                                Tunction="tyrosine kinase"
/note="txk belongs to tec family of tyrosine kinases"
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Mus musculus tyrosine kinase Txk mRNA, complete cds.
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/dev stage="5 week old"
1. .46
49. .1632
/function="tyrosine kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .2204
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C5"
/db_xref="taxon:10090"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mamm. Genome 6 (7), 476-480 (1995) 96059536
db_xref="taxon:10090"
                                                             cell_type="thymocyte"
tissue_type="thymus"
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                                                                                                               dev stage="adult"
....1680
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2193. .2198
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D43963.1 GI:604883
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MUSPTKRL18/c
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GRPTFALLOVLTEIAETW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          мUSKLK
Mus cookii resting lymphocyte kinase (RLK) gene, complete cds.
L35268
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Hu, Q., Davidson, D., Schwartzberg, P.L., Macchiarini, F., Lenardo, M.J., Bluestone, J.A. and Maiis. L.A.

Identification of RIK, a novel protein tyrosine kinase with predominant expression in the T cell lineage
J. Biol. Chem. 270 (4), 1928-1934 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="resting lymphocyte kinase"
note="predominant expression in T cell lineage; protein
yrosine kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Jan 14, 1995 this sequence version replaced gi:529439.
Original source text: Mus cookii (clone K9A) tetus thymus cDNA to
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
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protein tyrosine kinase; resting lymphocyte kinase.
Mus cookii (Cook's mouse)
Mus cookii
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MUSRLK/c
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Mus musculus (house mouse)

Nus musculus

Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bummalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 2342)

Nakayama, H. and Fujita, J.

Enhanced expression of multiple protein tyrosine kinases in the mouse regenerating liver: Isolation of PTK-RL-18, a novel cytoplasmic tyrosine kinase gene of Tec PTK family

Unpublished cytosine kinase gene of Tec PTK family

Engashiteuji, H.

Direct Submission

L. Submission

Submission

Submission

Submission

Submission

Submission

Submission

Syoto University, Clinical Molecular Biology; Shogoin Kawahara-cho 54, Sakyo-kw, Kyoto, Kyoto 66-850', Japan

(E-mail:hhigashi@virusl:virus.kyoto-u.ac.jp, Tel:81-75-751-3753, Fax:81-75-771-3753,
/translation="MILSSYSFOSVLCCCCRCSVOKROVRTOISLSREEELSEKHS
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GRPTFAELLQVLTEIAETW"
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Mus musculus PTK-RL-18 mRNA for protein tyrosine kinase, complete
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0.83;
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Matches 24; Conservative 0; Mismatches
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomyceteles; Dipodascaeae; Yarrowia.

Saccharomycetales; Dipodascaeae; Yarrowia.

CB Loases 1 to 4003362)

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Goffard,N.; Frangeul,L.; Aigle,M.; Anthouraf,V.; Babour,A.;

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                                             LOCUS CR382132 Accession CR382132
                                                                                              210000
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Yarrowia lipolytica CLIB99
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                                                              Fragment Name CR382132 00 CR382132 01 CR382132 02 CR382132 03 CR382132 04 CR382132 04
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CR382132_27
CR382132_28
CR382132_39
CR382132_31
CR382132_31
CR382132_34
CR382132_34
CR382132_34
CR382132_34
CR382132_35
CR382132_36
CR382132_37
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CR382132_07
CR382132_08
CR382132_09
CR382132_11
CR382132_12
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QRQRPWFAKLMGKTQSNRGGVQPSKRKPLPPLPQEPDDEXTQVKALYDFLPREPGNLA
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Pred. No. 0.86;
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100.0%; Pred. No. 0.83;
ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. No. 0.8
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                                                      codon_start=1
evidence=experimental
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/gene="PTK-RL-18"
                                  gene="PTK-RL-18"
     gene="PTK-RL-18
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Matches 24; Conserv
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Best Local Similarity
Matches 24; Conserv
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nes 24; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence split into Fragment Name Fragment Name AC013623 0 AC013623 2 AC013623 3 AC013623 4 Continuation 74 of 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fragment Name
AC013623 0
AC013623 1
AC013623 2
AC013623 3
AC013623 4
Continuation (3 of 5
                                                                                                                                                                                                                                                                                                          polyA_signal
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AC013623 2
WPCOMMENT
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Matches
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AC013623 3
WPCOMMENT
                    CDS
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Complement (19703. 20994)

Complement (19703. 20994)

Locus rag="YALIOFOOL76g"

Complement (join (19703. 20796, 20853. 20934))

Locus rag="YALIOFOOL76g"

Complement (join (19703. 20796, 20853. 20934))

Locus rag="YALIOFOOL76g"

Locus rag="Yaliofool76g"
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KGLSTFMSBMLETSALIKSATDKSLIIIDELGRGTSTYDGFGLAMAISEHIVKGMCFS
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VKFPTKVNMAKRAGELDDVNSGTGGKKASEDLVAGNKLLKEILTEWKSQIKGDEV
DGASQLLKTVVDKYKTQMEQNVFINDALASL"
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GSSNNAVDLAVCVOIVKYGKPCEGIINSSPRELYVKKTYVIVIKELSSYLASPDYEL
QDFATQFSELFKYISESLEBEGVPVLLTFULPSFRAYELNPVAPDTQKRIPFLDLEL
PELEQTLEVEFSDIEDBEVYVEEEFTPQFASTVSGVQKESLLDARKERLEKQKDDPFY
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/locus tag="YALIOF00198g"
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Saccharomyces carevisiae ORF YPL195W Alpha/gamma adaptin, start by similarity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX663616
Zebrafish DNA sequence from clone DKEY-287H22 in linkage group 7, complete sequence.
BX663616
BX663616.13 GI:47522521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 0.86;
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24; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          locus tag="YALI0F00176g"
'number=1
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Best Local Similarity
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BX663616/c
LOCUS
BX
DEFINITION Zel
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DCVQPSHSYVDTRRKSSGIPLEGDASIPTLISDPDKTTEDFKGGVNGNSLSQFPQE
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COMplement (14272. .15570)
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tr[Q]101161 Saccharomyces cerevisiae YOL054W, hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission

Submitted (01-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex -FRANCE (B-mail : seqref@genoscope.cns.fr -
Neb : www.genoscope.cns.fr)

This sequence is unfinished. Sequencing was performed at Genoscope and annotations were obtained by the genolevures Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Genoscope sequence ID : YALIOFCHR"
complement(13437. .14069)
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complement(13437. .14069)
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/note="unamed protein product; no similarity, possibly noncoding, hypothetical start"
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/strain="CLIB99"
/db xref="taxon:284591"
/chromosome="F"
Nature 430 (6995), 35-44 (2004)
                                                                 (bases 1 to 4003362)
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                                                                                                   Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                               AUTHORS
TITLE
JOURNAL
                                                                 REFERENCE
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gene

CDS

FEATURES

COMMENT

gene

CDS

ORGANISM

KEYWORDS

AUTHORS

JOURNAL

COMMENT

REFERENCE

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AL Submitted (20-10N-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:
Zifish-help@sanger.ac.uk Clone requests: clonerequestosanger.ac.uk
Zfish-help@sanger.ac.uk Clone requests: clonerequestosanger.ac.uk
Zfish-help@sanger.ac.uk Clone requests: clonerequestosanger.ac.uk
Zfish-help@sanger.ac.uk Clone requests: clonerequestosanger.ac.uk
During sequence assembly data is compared from overlapping clones
Where differences are found these are annotated as variations
Uncertain a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL, Sw., SWISSPROT; Tr., TREMBL, Wp., WORWPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep CH211-225JJ7 is
from a CHORI-211 BAC library
WECTOR: PARABAC2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VECTOR: prAREMACZ.1

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

This sequence is the entire insert of clone CH211-225JJ The true right end of clone CH211-23JILB is at 96893 in this sequence. Clone CH210-23JILB is at 96893 in this sequence. Clone darived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, Washu). For further information see better the left information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="Dr000087 repeat: matches 255. .674 of consensus"
complement(556. .661)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      554. .1032
note="Dr000087 repeat: matches 957. .1326 of
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'note="19.0 copies 3 mer TAA 114% conserved"
1114. .1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Wellcome Trust Sanger Institute
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/clone_lib="CHORI-211"
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Contact: zfish-help@sanger.ac.uk
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1. .192578
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                                                                          HTG; zinc finger.
Danio rerio (zebrafish)
                                                                                                                                                             Danio rerio
                                       AL732455.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with ris sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information the being a found at the cloud at the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL732455
Zebrafish DNA sequence from clone CH211-225117 in linkage group 7 Contains part of a novel gene for a zinc finger protein, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-287H22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                  Submitted (19-72-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Clone nequests: clonerequest@sanger.ac.uk Om May 19, 2004 this sequence version replaced gi:47109759.
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 this is found the longest good quality representation will be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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/db xref="taxon:7955"
/clone="DKEY-287H22"
/clone_lib="DanioKey"
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                                                    Danio rerio (zebrafish)
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                                                                                                    Danio rerio
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Query Match

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FEATURES

Matches

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DEFINITION

LOCUS

RESULT 70 AL732455

	/note="ACROBAT1 repeat: matches 776842 of consensus"	rear tearer
repeat_region	1275)	
repeat_region	/note="broup340 repeat: matches 135196 of consensus" complement(12721327)	repeat_regi
repeat region	/note="Dr000403 repeat: matches 166 of consensus" complement(1369 1617)	repeat_regi
repeat region	/note="Dr000262 repeat: matches 5284 of consensus" 1620. 1631	repeat_regi
	/note="12.0 copies 1 mer T 24% conserved" 1659. 1731	repeat_regio
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	/note=:27.7 /note=:2.0 copies 6 mer TTAGTA 24% conserved" 1774 1795	repeat_region
	/note="2".2" /note="2".2" copies 8 mer TTTAAAGA 26% conserved" 1998 - 2008	repeat_regic
region	/note="2.8 copies 4 mer AGAT 22% conserved" 20172031	repeat_regio
	/note="3.8 copies 4 mer CAGG 30% conserved"	repeat_regic
region	Jobe="HATI_DR repeat: matches 575647 of consensus" 2103 2200	repeat_regic
region	/note="HAT1_DR repeat: matches 555660 of consensus" 21352211	repeat_regic
region	/note="Dr000309 repeat: matches 2. ,78 of consensus" 23972412	repeat_regic
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repeat region	/note="7.0 copies 2 mer TC 28% conserved" 3063, .3074	repeat_regic
repeat region	/note="2.4 copies 5 mer ATATG 24% conserved" 3280. 3407	repeat_regic
repeat region	/note="HAT1 DR repeat: matches 521659 of consensus"	repeat_regic
	/note="Dring00309 repeat: matches 269 of consensus" 3408	repeat_regio
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	/note="2.0 copies 6 mer AAACAG 24% conserved" 36293641	repeat_regio
	/mote="13.0 copies 1 mer T 26% conserved" 36873696	repeat_regio
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repeat region	/note="2.2 copies 6 mer TGATTC 26% conserved" 3914 3447	repeat_regio
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	/note="3.1 copies 7 mer ACACTAA 23% conserved" 4274 4346	Query Match Best Local Simi
	/note="Dr000236 repeat: matches 358433 of consensus"	Marches 24
repeat region	/note="12.0 copies 6 mer GTTTCT 24% conserved"	
	1.00: "JASITAL DR repeat: matches 1186 of consensus"	Db 6479 GAA
	Journal of the Construction of	RESULT 71
repeat region	Comprement(3134: .3239) /note="UNM11TAL_DR repeat: matches 1130 of consensus" 6413 - 6433	
repeat region	Jaco: 1212. 1212. Jacobies 5 mer TACAT 22% conserved" Component (5,99% 5,681)	DEFINITION MUS IN PROGRE
repeat region	/note="Dro000009 repeat: matches 770. ,857 of consensus" 5803 = 824	VERSION AC099
region	/inch="2.3" copies 9 mer ACAGAATGG 35% conserved" 62246233	ORGANISM Mus m Eukar
	// note="2.5 copies 4 mer ACAA 20% conserved"	REFERENCE 1 (b

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199698 10 134365951
3; HTGS PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.

3) musculus (house mouse)

3) musculus (chordata; Craniata; Vertebrata; Euteleostomi; aryota; Metazaa; Chordata; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 222930)
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9430. 9441
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9447. 9466
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10601. 10611
/note=="0.8 copies 4 mer CTTC 22% conserved"
10867. 10885
/note=="0.2 copies 6 mer AGGA 21% conserved"
10867. 10885
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6238. .6253

Anote="16.0 copies 1 mer A 32% conserved"

6626. .6635

/note="2.5 copies 4 mer GAAT 20% conserved"

7338. .6760

/note="7.7 copies 3 mer TCC 39% conserved"

complement (7233. .7249)
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Signature, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Cooke, P., Dakrellano, K., Collins, S., Collymore, A., Cooke, P., Parriago, K., Collins, S., Collymore, A., Cooke, P., EitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Govette, M., Gardon, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Karatas, A., Karatas, R., Meldrim, J., MacCarn, C., MacGonald, P., Major, J., Marquis, N., Matthews, C., MacGonald, P., Major, J., Marquis, N., Matthews, C., Nacan, C., MacGonald, P., Major, J., Marquis, N., Matthews, C., Norman, C., MacMan, C., Reters, R., Meldrim, J., Norman, C., M., O'Connor, T., O'Donnell, P., Nolly C., Connor, T., O'Donnell, P., Nolly C., Stause, S., Schupback, R., Stanss, N., Subramanian, A., Sancis, R., Stause, S., Schupback, R., Stanss, N., Subramanian, A., Sancis, R., Stanss, N., Subramanian, A., Tasiame, A., Tasiame, J., Vassiliev, H., Travis, N., Vassiliev, H., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G. Sannon, J., Zambek, L., Zimmer, A., and Zody, M.

Strauss, N., Subramanian, A., Tasiams, J., Yegiaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Yugh, N., Yugh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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s: gap of 100 bp
s: contig of 100 bp
7: contig of 100 bp
7: contig of 100 bp
8: gap of 100 bp
8: contig of 5291 bp in length
8: gap of 100 bp
9: contig of 4328 bp in length
8: gap of 100 bp
7: contig of 4328 bp in length
6: gap of 100 bp
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project_Information
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of 37218 bp in length
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of 3759 bp in length
100 bp
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 5, clone RP23-41509
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Eiren, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,

Brown, A., Camarata, J., Callymore, A., Cook, A.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,

Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,

Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,

Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,

Hagos, B., Headrod, A., Kartas, A., Kells, C., Levine, R., Liu, G.,

Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,

MacLean, C., Madonald, P., Major, J., Marquis, N., Matthews, C.,

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Mcarthy, M., McMan, P., McKennan, V., McPheeters, R., Meldrim, J.,

Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,

Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,

Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Schupback, R.,

Saman, S., Severy, P., Santos, N., Teigilio, J., Young, G.,

Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Topham, K., Travers, M., Travis, N., Trigilio, J., Young, G.,

Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

All Shesearch, 320 Charles Street, Cambridge, MA 02141, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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222930: contig of 27854 bp in length.
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0.87;
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TITLE JOURNAL REFERENCE AUTHORS

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complement(156. .186)
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187 _ 229</pre>
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complement(2225. .2468)
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complement(235. .2468)
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complement(230. .390)
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site:Mbol"
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/rpt_family="AT_rich"
7481. 7504
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complement(1509..165
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                                         FEATURES
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Research, 320 Charles Street, Cambridge, MA 02141, USA

Anderson,M., Arachchi,H.M., Barna,N., Bastian,V., Bloom,T., Boduslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cooke,P., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dodley,K., Dorniel,L., Brickson,J., Farchson,A., Rander,B., Brickson,J., Farcham,L., Grand-Pierre,N., Halfez,N., Hagoplan,D., Hagos,B., Hall,J., Horten,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Indblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., Machen,C., Machad,L., Mihova,T., Malenga,V., Murphy,T., Naylor,J., Nguyb,C., Naiol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Peierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassillev,H., Venkaeraman,V.S., Wiell,R., Volk, Wilson,B., Wu,X., Wwman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. Direct Submission
                                                                                                                                                                                                                                                                                                                All Submitted (12-JUN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases I to 224556)

8 Intern, B., Nusbaun, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T. Boqualavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Corum, B., Dehrellano, K., Diaz, J. S., Dooley, K., Dorisi, L., Erickson, J., Faro, S., Ferreira, P., Firzderald, M., Gage, D., Galagan, J., Gardyna, S., Ferreira, P., Firzderald, M., Hafez, N., Hagosh, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Maccan, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Mahdid, J., Mortul, R., Norbu, C., O'Connor, T., O'Donnell, P., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachuers, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Tavers, M., Wanan, D., Young, G., Zembek, L., Zimmer, A. and Zody, M., Whirthed, (11-min, 2004) M., Scholl, M., Milch, M., Milson, B., Nord, M., Milch, M., Milson, B., Nord, C., Stender, S., Schupbeck, L., Zimmer, A. and Zody, M., Schheir, E., Schupbeck, L., Zimmer, A. and Zody, M., Schheir, E., Schupbeck, L., Zimmer, A. and Zody, M., Schheir, E., Schupbeck, L., Zimmer, A. and Zody, M., Schupier, C., Subrater, S., Schupbeck, L., Zimmer, A., and Zody, M., Schupier, C., Subrater, S., Schupbeck, L., Zimmer, A. and Zody, M., Schupier, C., Subrater, S., Schupbeck, L., Zimmer, A. and Zody, M., Schupier, C., Subrater, S., Schupbeck, L., Zimmer, A. and Zody, M., Schupier, C., Subrater, M., Milson, B., Schuper, E., Schupbeck, L., Zimmer, A. and Zody, M., Baharither, M., Milson, S., Schupbeck, L., Zimmer, A. and Zody, M., Schupier, C., Subrater, M., Schup, S., Schupbeck, L., Zimmer, A., and Zody, M., Schup, G., Schup, S., Schupbeck, L., Zimmer, A., and Zody
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Myguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K., Phunkhang, P., Pterre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Spencer, B., Stange-Thomann, W., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Center: Whitehead Institute/ MIT Center for Genome Research
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------- Froject Information
Center project name: 1,18799
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E (bases 1 to 289405)

E (bases 1 to 289405)

Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Gararata,J., Camapoplano,A., Clangell,Y., Colangelo,M., Collins,S., Collymore,A., Cocke,P., Detrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karates,A., Larocque,K., Lamazares,R., Landers,T., Landers,T., Marthews,C., McClann,C., MacGonald,P., McKernan,K., Marthews,C., McCatthy,M., McEwan,P., McKernan,K., McThews,C., McCatthy,M., McKernan,R., McRenan,C., McConald,T., Obonnell,P., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Resetta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Rolley,R., Schauer,S., Schubback,R., Scandas,S., Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassillev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,J., Y., Vo,W., Y., Wyman,J., Y., Wyman,J., Y., Wyman,J., Y., Wyman,J., Y., Wyman,J., Y., Wyman,J., Y., Wywan,J., Y., Wywan,J., Y., Young,G., Zainoun,J.,
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Burren, B., Nusbaum, C., Lander, B., Abouelleil, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguelavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chopel, Y.,
Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
Macdonald, P., Maror, J., Manning, J., Matthews, C., McCarthy, M.,
Maldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schubba, K., Senery, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
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Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 5, clone RP23-6518
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                                                                                                                                    Score 24; DB 10; Length 224556;
Pred. No. 0.87;
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Mus musculus chromosome 5 clone RP23-6518 map 5, 'PROGRESS ***, 11 unordered pieces.
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Mus musculus (house mouse)
                                                                                                                   1.0%; Scc.
100.0%; Pred. No.
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Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
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Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. Direct Submission
                                                                                              Submitted (15-APR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 25, 2003 this sequence version replaced gi:30018220.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
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28099; gap of 100 bp
36806; gap of 100 bp
45491; contig of 8585 bp in length
45591; aga of 100 bp
48670; contig of 8079 bp in length
48770; gap of 100 bp
52431; contig of 351 bp in length
52431; gap of 100 bp
                                                                                                                                                                                                                                                                                                                        Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L11591
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of 11546 bp in length
100 bp
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Location/Qualifiers
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: contig of 41535 bp i
gap of 100 hr
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Web site: http://www-seg.wi.mit.edu
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100.0%; Pred. No. 0.87;
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Sequence 127 from Patent WO2004078783.
CQ871636
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Center clone name: 65_I_8
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                                                                                                                      Murphy, F.J., Sheehan, D.E., Keating, K.E., Hayes, I.E. and Seera, L.E. Enzymes involved in apoptosis
Patent: WO 2004078783-A 127 16-SEP-2004;
Elix Therapeutics Lid (IE)
Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 595)
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Whitehead Institute for Biomedical Research, Center for Genome
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1.0%; Score 23; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 0; Indels
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/map="- 5 22-540 71845760-71846277"
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320 Charles Street, Cambridge, MA 02141, USA
181: 6172521477
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="QPCR primer"
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synthetic construct
other sequences; artificial sequences.
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Primer A: None
Primer B: None
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Mus musculus
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G94809.1 GI:22745565
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Query Match 1.0%; Score 23; DB 11; Length 595;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps
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Search completed: March 25, 2005, 20:35:15
Job time : 9731 secs

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us-09-436-184-3.oligo.rst

CN274513 170006000 BP28261 BP38261 B0989709 AGENCOURT B0722578 AGENCOURT AU13266 AU13266 BU502606 AGENCOURT BF962729 QV2-NN004 BE982739 T70004243	AL700393 DKFZp686K BU502544 AGENCOURT AL120973 DKFZp6762H CM481470 hw08b65.y BF943222 QV2-NN004 AU138660 AU138660 BQ18665 CM0-CT054 BQ278565 AGENCOURT BP962946 QV2-NN004 BQ639558 hel7004.y CNS6821 T7000601 CM483754 hw36h12.y BQ339559 QV2-NN200 BQ339559 QV2-NN200	BEO94330 QUZ-NN200 BEO94010 PMO-BT065 BEO94010 PMO-BT065 BEO94010 PMO-BT065 CN31352 U1-CP-RN0 CN36826 170004243 BE37659 601485742 ALS ALS ALS AGGS OF ALS AGGS OF AGGS	MAGE 200 AGENCOURT CN36820 170005336 BN158224 603036396 CR769476 DRF29469H AR652752 wb65201.x BX374107 BX374107 CN258115 170005318 BG701542 602682786 BG701542 602682786 BG701542 60243130 BG332543 60243432 BG332543 60243432 BG37347 CML CN010 BH3193485 GC9947432 BG977347 CML CN010 BH31655 GWL CN010 BF911655 GWL CN011 BF911655 GWL CN011 BF911655 GWL CN011 BF911659 GWL CN011 BF914358 AGENCOURT CF619299 AGENCOURT CF619299 AGENCOURT CF619299 AGENCOURT
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on 5.1.6 5 Compugen Ltd. 1 1 Search time 6778 Seconds (without alignments) (without alignments) 13051.248 Million cell updates/sec	ttgggaaactctggaga es : 68479088	results predicted by chance to have a to the score of the result being printed, of the total score distribution. SUMMARIES ID	00000000000000000000000000000000000000
GenCore version Copyright (c) 1993 - 2005 nucleic - nucleic search, using sw model non: March 25, 2005, 16:47:45 ; Se (w	Title: Perfect Score: 2324-36-184-3 Sequence: 1 cggaccgtgcaatggcccag	g first 10 est1: * 'est2: * 'htc: * 'htc: * 'st6: * 'gs81: * 'gs81: * 'gs81: * 'gs82: * 'gs82: * 'gs82: *	1803 77.6 2126 9 AY405267 766 33.0 1050 4 BM806632 73.0 1050 4 BM806632 628 25.9 9 18 BM700814 628 27.0 9 182 7 CK74966 603 25.9 9 18 BM700814 628 24.9 9 18 BM700814 658 24.9 9 18 BM700814 658 24.4 603 5 BP376604 558 24.2 883 5 BP376604 558 23.4 6511 2 AW906828 531 23.3 1011 5 BP270196 531 22.8 765 6 CD643948 517 22.2 17 5 BP270196 517 22.8 765 6 CD643948 517 22.8 765 6 CD643948 717 22.8 765 6 CD643948 717 22.8 765 6 CD643948 717 22.8 718 7 CM368829 441 19.8 770 7 CM368829 4451 19.8 770 7 CM368829 758 758 758 758 758 758 758 758 758 758

### RESULT 1 ***ALIGNMENTS**	634 CCGAGCATAGTTACCACGTGGAAGACAGTTTCACAAGACTGTAATCAGGATATGGAAG 693 [983 AAAAGAAGCCTAAACTTTTAAATAATTAAAGAAGACTATTAAAGCTGAACTTGATGCTG 1042 1054 CAGAAAAACTCCGTAAAAGGGGAAAAATTGAGGAAGCAGGAATGCATTTAAAGAACTGG 1013 1043 CAGAAAAACTCCGTAAAAGGGGAAAAATTGAGGAAGCAGTGAATGCATTTAAAGAACTAG 1113 1114 TACGCAAATACCCTCAGAGTCAACAGAAGAAGAGAAGAG		AACTTGCCAATGATACTTCCTAAAAATGACCTTGGCGGGGATACCTCTTGATGATACTTCCCAATGATACTTCCCAATGATCCTTTAAAAAATGACCTTGGCGGGGATACCTCTTGATGATACTTCTTTTCCCAATGATTATCAAGAGTGCCTTGGCGGGGATACCTCTTGATAGATA
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1 L L L L L L L L L L L L L L L L L L L	9.7 404 4 BG979400 BG979400 CM4 9.6 549 1 AA176259 AA176259 ZP2 9.5 504 6 CD675871 CD675871 fs2	AY405267 2126 bp DNA linear GSS 16-DEC-2 Homo sapiens ASPH gene, VIRTUAL TRANSCRIPT, partial sequence, Genomic survey sequence. AY405267.1 GI:39761241	GSS. Homo sapiens (human) Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2126) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.		Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and orderin them based on alignment. Location/Qualifiers i. 2126 /organism="Homo sapiens" /nol type="genomic DNA" /db xequencapenanco DNA"	/locus_tag="HCM2167" 77.6%; Score 1803; DB 9; Length 2126; 3; Conservative 0; Mismatches 0; Indels 0; Gaps 3; Conservative 0; Mismatches 0; Indels 0; Gaps GACTTAAAGAGAGTCTTCAGAGCCAGCAGCCCCAGAAGAGGCTGAGCCACAA [

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1085 bp mRNA linear EST 06-MAY-2004
BX459083 Homo sapiens cDNA clone CS0DE012YB13
5-PRIME, mRNA sequence.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1085)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                         181 TTGATGCTGCAGAAAAACTCCGTAAAAGGGGAAAAATTGAGGAAGCAGTGAATGCATTTA
                                                                                         ATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAG
                                                                                                                                                     925 AACAGCAGGAAGTACCACCAGAAACAAATAGAAAAACAGATGATGCAGAACAAAAGCAA
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                             DB 4; Length 1050;
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                       Query Match 33.0%; Score 766; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 766; Conservative 0; Mismatches
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BX459083.2 GI:47064816
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I (Basea I to 160.)

I (Basea I to 160.)

National Institutes of Health, Mammalian Gene Collection (MGC)

Notional Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mill.inh.gov,

Contact: Robert Strausberg, Ph.D.

Email: Capbs-r@mill.inh.gov

Tissue Procurement: ArCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be from through the I.M.A.G.E. Consortium/LLNL at:

Lond distribution: MGC clone distribution information can be frutp://image.llnl.gov

Plate: LLAM1258 row: k column: 24

High quality sequence stop: 649.

Location/Qualifiers

// Lissue Lype="melanotic melanoma"

// Clone lib="MIM MGC 72"

// Note="Organ: Bkin; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr. Sechnologies."

Fechnologies."
                                                                                                                                                   1882
1883 TCACGCTGTGGCAGCAAGGAAGAAGAATGAAAATGCCTGCAAAGGAGCTCCTAAAAACCT 1942
                                                                                                                                                                                                                                                            2003 CCATCATGCACCCCGGGACTCACGTGGCCGCACACACACGCCCACAAACTGCAGGCTCC 2062
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E543030 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548943
                                               AGTCTTTAGAAAGAAACTGGAAGGTTAATCCGAGATGAAGGCCTTGCAGTGATGGATAAAG
                                                                 1894 TCACGCTGTGGCAGCAAGGAAGAAGAAATGAAAATGCCTGCAAAGGAGCTCCTAAAAACCT
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5', mRNA Sequence.
BM806632
BM806632.1 GI:19123455
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/call type="Ycomacn"
/call type="Floating aggregates"
/call type="Floating aggregates"
/call thes="Yopubus"
/call the last stomach; Vector: pT218RPI; Site 1: EcoRI;
Site 2: Not!; The pOly (A) + RMA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNM was ligated with DNA-RNA linker including EcoR is the by treatment of T4 RNA ligase and the first strand CDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The CDNA vector was adjusted to alwa strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli TOploR' by electroporation method. The cDNA libraries constructed by this method are full-length enriched CDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                           BM790814 689 bp mRNA linear EST 05-MAR-2002 K-EST0070696 S21SNU520 Homo sapiens cDNA clone S21SNU520-16-C08 5', mRNA sequence.
BM790814
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821
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 689)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                             762 GATACAGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA
                                                                                          822 AATGAAGGGATAGAAATCACAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Booun-dong Yuseong-gu, Daejeon 305-333, South Korea
Fax: +82-860-44409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21C Frontier Korean EST Project 2001
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="S21SNU520-16-C08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: yongsung@mail.kribb.re.kr
Plate: 16 row: C column: 08
High quality sequence stop: 689.
Location/Qualifiers
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//tissue type="PLACENTA"
//tissue type="PLACENTA"
//clone lib="Homo sapiens PLACENTA"
//one lib="Woctor: PCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
the Not I and SCORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
              Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31027087.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
S. rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-loigo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 gagagarcracricagagccagcagrcccgccagaagaggcrgagccacacacreagccc
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                                                                                                                                                                                                                                                      division of Invitrogen.
This sequence belongs to sequence cluster 4537.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE012CA07QP1&c=4537.r.
Location/Qualifiers
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31.6%; Score 734; I
Best Local Similarity 99.9%; Pred. No. 0;
Matches 784; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/organism="Homo sapiens"

/mol_type="mcNA"

/mol_type="mcNA"

/db_xref="taxon:9606"

/clone="UI-H-EDI-axp-c-22-0-UI"

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/clone=lib="NGI CAPP EDI

/clone=lib="NGI CAPP EDI

/note="Organ: Left Public Bone; Vector: pT7T3-Pac

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/clone lib="NGI CAPP EDI is a normalized CDNA library

/clone lib="NGI CAPP EDI is a normalized CDNA library

/containing the following tissue(s): Chondrosarcoma cell

line CSS: The library was constructed according to

/containing the following tissue(s): Chondrosarcoma cell

line GSS: The library was constructed according to

/containing the following tissue(s): Chondrosarcoma

line GSS: The library was constructed according to

/containing the following tissue(s): Chondrosarcoma

ligo-dr prime containing a Not I site. Double stranded

CDNA was ligated to an ECOR I adaptor, digested with Not

oligo-dr prime containing a library tag sequence that is

liret-strand CDNA contains a library tag sequence that is

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National Cancer Institute / NIH
Bldg. 31 Kml0AnO Betheada, MD 20892
Bmail: ggapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
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1 (basea 1 to 78).

NCI-GAAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                     1219 AGACCTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGCAGACCTGCAGAGCTGAGTT
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Inpublished (1997)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
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                                                                        GGTTTATGGTGGATTGCATTGCTGGGCGTCTGGACTTCGTAGCTGTCGTTTGGTTTGATC 240
                                                                                                                                       TICITGACTATGAGGAAGTICTAGGAAAACTAGGAAICTATGAIGCTGAIGGIGAIGGAG 300
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                          601 AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGG 654
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17000532543418 GRN_ES Homo sapiens CDNA 5', mRNA sequence.
CN258120
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230 Constitution Drive, Menlo Park, CA 94025, USA
191: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 729 Std Error: 0.00.
Location/Qualifiers
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/mol_type="mRNA"
/mol_type="mRNA"
/dolone="IMAGE:6147375"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/lab_host=="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; cloned unidirectionally. Primer: Oligo dT.
Average insert size_2 kb. Library constructed by Life
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14 MGC.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                             94 GCCAAAGGTCTCTTCCTGCCTGAGGATGAAACCTGAGGGAAAAAGGGGACTGGAGCCAG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapber@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
Tissue Procurement: ATCC/DCTD/DTP
Tissue Procurement: ATCC/DCTD/DTP
TONA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LiAMl3477 row: b column: 16
High quality sequence stop: 634.
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GAGCTTGGGCACAGAGAGGACACTTTGCATCTGTCTGGCAACGCTCACTCTAAAGACAACGTA
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                                                                                   1696 GCTCACTCTACAATGTGAATGGACTGAAAGCACAGCCTTGGTGGACCCCAAAAGAAACGG 1755
                                                                                                                                                                         TTGCAGTGATGGATAAAGCCAAAGGTCTCTTCCTGCCTGAGGATGAAAACGTGAGGAAA 1875
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868 bp mRNA linear EST 04-SEP-2002
AGENCOURT_7953975 NIH_MGC_68 Homo sapiens CDNA clone IMAGE:6010847
BU175716
                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   543 TGTGGCATCCGGAACTGACACCACAGCAGAGACGCAGCCTTCCAGCAATTTAGCATGAAT 602
from undifferentiated hES cell lines H1 (p22), H7 (p29), and H9 (p26) maintained in feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomosopiums Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases Euthoria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Cgapba-rémail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
                                                                                                 1756 GCTACAGAGTTAGTAAAGTCTTTAGAAAGAAACTGGAAGTTAATCCGAGATGAAGGCC
                                                                                                                                          63 GCTACACAGAGTTAGTAAAGTCTTTAGAAAGAAACTGGAAGTTAATCCGAGATGAAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                       .176 CCTTTGAGCACGAGGAAGGATGCCTCATCTTTCCGGCTGATATTCATCGTGGATG
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                                           Score 578; DB 7; L
Pred. No. 1.2e-298;
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                                         24.9%;
Local Similarity 99.8%;
les 628; Conservative
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1..868 // Constitution Sepiens // Conganism=Homo sapiens // Moi type="mRNA" |
| Ab xref="taxon:9606" |
| Ab xref="taxon:9606" |
| Alb host="bH10B (phage-resistant)" |
| Alb host="bH10B (phage-resistant)" |
| Anote="Organ: lung' Vector: pCWV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1811
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                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Flate: LLAM13199 row: i column: 24
High quality sequence stop: 547.
                                                                                                                                                                                                                                                                                                                                                                                                  Length 868;
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Pred. No. 4.4e-298;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                              tch 24.8%;
al Similarity 99.8%;
627; Conservative 0
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1282 AGCGICCCTCACACACCAACTTTCTAGGICATATGAGAGGTICCCTGCTTACCCTGC 1341
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                                                                                                          BP364957
BP364957 Sugano cDNA library, fetal lung fibroblast TIG Homo sapiens cDNA clone TIR05529, mRNA sequence.
                                                                                                                                                                                                                                                                                            Lusaca, L.V. Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Contact: Yuteka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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381 CACCTAATGATGGCTTTGCTAAAGTCCATTATGGCTTCATCCTGAAGGCACAGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="fetal"
/clone_lib="Sugano cDNA library, fetal lung fibroblast
TIG"
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100.0%; Pred. No. 1.4e-29
tive 0; Mismatches 0
1341 CAGAGATTAGTTCAACTATTTCCCAATG 1368
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/organism="Homo sapiens"
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/cell_type="fibroblast"
/cell_line="TIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TIR05529"
                 576 CAGAGATTAGTTCAACTATTTCCCAATG
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     BP336604 Sugano cDNA library, coronary artery smooth muscle cell Homo sapiens cDNA clone SMR06083, mRNA sequence.
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                                                                                                                                        E.C. S. S. S. S. S. Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 603)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushina-Sugano, J., Nakai, K. and Sugano, S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 111-1718 (2004)

Department of Wirology
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="skan:9606"
/clone="SMR06083"
/clone="SMR06083"
/clone="smronary artery"
/cell_type="smooth muscle cell"
/clone=lb="sugano cDNA library, coronary artery smooth muscle_cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTGAGGATGATTTGGCTGAGAAGAGGAAGTAATGAGGTGCTACGTGGAGCCATCGAG
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                                                                                                                                                                                                                                                                                                              Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp.
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100.0%; Pred. No. 2.9e-293;
:ive 0; Mismatches 0;
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Qy 1522 TTGCTGAGAGCATCCCATATTTAAAGGAAGGAATAGAATCGGAGATCCTGGCACTGATG 1581 bb 441 TTGCTGAGAGCATCCCATATTTAAAGGAAGGAATTGAATCCGGAGATCCTGGCATGATG 500 Qy 1582 ATGGGAGATTTTATTTCCACCTGGGCATCCAAAGAGGTTCGGAACAAAGAGCAT 1641 bb 501 ATGGGAGATTTATTTCCACCTGGGGATGCCATGCGAGGGTTGGGAACAAAAGAGGCAT 560 Qy 1642 ATAAGTGGTATGAGCTTGGGCAC 1664 Db 561 ATAAGTGGTATGAGCTTGGGCAC 1664 Db 561 ATAAGTGGTATGAGCTTGGGCAC 1864	11 2 AU130952 ION AU130952 NT2 BEQUENCE ON AU130952	VERSION AU130952.1 GI:10991306 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens ELMATYOTA; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 859) AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Zamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isocai,T.	cDNA project ed (2000) logal Laboratory earch Institute arch Essarazu, Chiba 292-0812, Japan 38-52-3978 38-52-3976 cDNA project; 5'- & 3'-end one pass sequencing:	Research Institute; CDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute. FEATURES Location/Qualifiers 1. 0859 / Organism="Homo sapiens" / Mol Lype="mRNA" / db xref="taxon:966" / coll rype="textcoarcinoma" / call libe="NTPRE" / call libe="	//Caraline="NAT2R9" //Clone lib="NT2R9" /note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction" Query Match	013 AAATAAATTIGATAAGACTATTAAAGCTGAACTTGATGCTGCAGAAAAACTCGTAAAAG 10

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/tissue type="PLACENTA"
/close lib="Homo sapiens PLACENTA"
/close lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
/note="Vector: pCMVSPORT 6; lst strand cDNA was digested with Not I and cloned
double-strand cDNA was digested with Not I and cloned
the Not I and BCORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                   Contact: Genoscope Genue National de Sequencage Contact: Genoscope - Centre National de Sequencage Contre Gaston Cremieux, P5706 - 91057 EVRY cedex - FRANCE 2 rue Gaston Cremieux, FP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-coligo(dT) Primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a
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                                                                                                                                                        division of Invitrogen.
This sequence belongs to sequence cluster 4537.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CLOBA007ZCO4RP1&c=4537.r.
Location/Qualifiers
 gi:30635043
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May 13, 2003 this sequence version replaced
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larity 99.3%; Pred. No. 1.1e-278;
Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/db_xref="taxon:9606"
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                              /dev_erage="Adult"
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/note="Corgan: breast_normal: breather by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Homo sapiens
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Li, Chaese, Lto 1011)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length, CDNA libraries and normalization
Unpublished (2001)
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Pred. No. 8.3e-280;
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                xref="taxon:9606'
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0; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  581 bp mRNA linear EST 16-SEP-2004
DP266690 Sugano cDNA library, thyroid JTH Homo sapiens cDNA clone
DP266690
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/organism="Homo sapiens"
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Homo sapiens
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B. (basea 1 to 2)

B. Enandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

L. Nat. Biotechnol. 22 (6), 707-716 (2004)

Contect: Brandenberger R

Regenerative Medicine

Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Fax: 650 473 760

Email: rbrandenberger@geron.com

Insert Length: 589 Std Error: 0.00.
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000551862302 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
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/mol type="mRNA"
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/db Xref="taxon:960"
/tisue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone l1b="eRN EB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hBS cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
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CN258117.1 GI:47274531
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/mol_type="mRNA"
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/tissue_type="Embryonic Stem cells"
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (Dases I to 582)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous

Sequence comparison of human and mouse genes reveals a homologous

Lock structure in the promoter regions

Lock structure in the promoter regions

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@lma.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1711 TGAATGGACTGAAAGCACAGCCTTGGTGGACCCCCAAAAGAAACGGGCTACACAGAGTTAG 1770
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                                                             Treaagcerceacacaacaarrerceacarcarrececacacarrece
                                                                                                     225 CIGCAGAGATTAGTICAACTATTCCCAATGATACTTCCTTAAAAAATGACCTTGGCGTG
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I (bases 1 to 765)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

Office of Cancer Genomics

National Cancer Institute / NIH

Bidg. 31 RmlOAO7 Betheda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Irene Ginis and Mahendra Rao, NIA

CDNA Library Preparation: Vulan Piao and Minoru Ko

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC c

can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: NDAM511 row: a column: 24

High quality sequence stop: 605.
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AGENCOURT_14550808 NIA Human H1 Embryonic Stem Cell cDNA Library
(Long) Homo sapiens cDNA clone IMAGE:30425975 5', mRNA sequence.
CD643948
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1830
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2131 AGACCAGGACCTGGGAGGAAGGCAAGGTGCTCATCTTTGATGACTCCTTTGAGGAGG
                                                                                                                                                                                                                                     CCTGTACCTTACTAGAAAAGTTCCCCGAGACAACAGGATGCAGAAGAGGACAGATCAAAT
                           301 CCTGTACCTTACTAGAAAGTTCCCCGAGACAACAGGATGCAGAAGAGGACAGATCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAAGTCTTTAGAAAGAAACTGGAAGTTAATCCGAGATGAAGGCCTTGCAGTGATGGATA
                                                                                                   AAGCCAAAAGGTCTTCCTGCCTGAGGATGAAAACCTGAGGGAAAAAGGGGAACTGGAGCC
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Query Match
Best Local S:
Matches 517
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                                                                                                                                                                                                                   RESULT 18
BX479249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
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                                                                             /LONGO W. Company of the control of co
/cell_line="WA01"
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/clone_lib="NIA Human Hl Embryonic Stem Cell cDNA Library
(Long)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACA 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACTCTAGAAAA 823
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579; Conserva
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Best Local S:
Matches 579,
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517 bp mRNA linear EST 04-SEP-2003
DKFZp686L22209_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686L22209_5', mRNA sequence.
BX479249
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Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
EST (Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., et al.)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert clone from 5. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Center for Biotechnology Ltd., Braunschweig/Germany) within the CDNA sequencing consortium of the German Genome Project.

No 81 sequence available.
This clone (DKFZp686L22209) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlotterburg, GERMANY; Email: clone@rzpd.de.
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          943
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 517)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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/note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
                                  884 ACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          926 ACAGCAGGAAGTACCACCAGAAACAAATAGAAAAACAGATGATCCAGAACAAAAGCAAA
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                                                                                                            944 AGAAACAAATAGAAAAACAGATGATCCAGAACAAAAAGCA 983
                                                                                                                                                                             591
                                                                                                                                                  552 AGAAACAAATAGAAAAAACAGATCCAGAACAAAAGCA
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22.2%; Score 517; DB 5; Le
al Similarity 100.0%; Pred. No. 7.8e-266;
517; Conservative 0; Mismatches 0;
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ISM Homo sapiens

Homo sapiens

Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Catarrhin; Hominidae; Homo.

CE 1 (bases 1 to 711)

Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,

Ii,Y., Xu,C., Fang,K., Guegler,K., Rao,M.S., Mandalam,R.,

Ichkowski,J and Stanton,L.W.

Transcriptome characterization elucidates signaling networks that

control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

Geron Corporation Drive, Menlo Park, CA 94025, USA

Trais 650 473 7760

Email: rbrandenberger@geron.com

Insert Length: 711 Std Error: 0.00.
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/note="oligo dT_primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
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                                                                                                                                                                                                                              241 ITGITGACTATGAGGAAGTICTAGGAAAACTAGGAAICTATGAIGCTGAIGGAGGAG
                                                                                                                                                                                                                                                                         153 TTGTTGACTATGAGGAAGTTCTAGGAAACTAGGAATCTATGATGCTGATGGTGATGGAG
                                                                                                                                                                                                                                                                                                                                       ATTITIGATIGTIGGATIGATIGCCAAAGTTTTATTAGGACTTAAAGAGAGATCTACTTCAGAGC
                                                                                                                                                                                                                                                                                                                                                                       421 AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG
                                       gerrrangergarracarracacarcrasacarcraracrarcrarracrrarracrra
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17000418219954 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
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CN368832.1 GI:47368766
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(Dasse; 1 to 721)

(In Interpolate; Manalian Gene Collection (MGC)

(In Mational Institutes of Health, Mammalian Gene Collection (MGC)

(Contact: Robert Strausberg, Ph.D.

(Email: cgapbs-remail.nih.gov

(Tissue procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Sequencing by: Incyte Genomics, Inc.

CDNA Sequencing by: Incyte Genomics, Inc.

CLONG distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Righ quality sequence stop: 719.

High quality sequence stop: 719.
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="INMAGE:5138622"
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/clone lib="NIH MGC_12"
/nofe="Organ: cervix, Vector: pCMV-SPORT6; Site_1: Not1;
/note="Corgan: cervix, Vector: pcm, Vec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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602996326F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:5138622 5',
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                                                                                                                                                                                         TCGCTCAGACAGGCAACTATTCTAGGTCATATGAGAGGTTCCCTGCTTACCCTGCAGAG 1345
                                                                                                                                                                                                                                                                                                  1346 ATTAGTICAACTATTICCCAATGATACTICCTTAAAAAATGACCTIGGCGTGGGATACCT 1405
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CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                 1406 CTTGATAGGAGATAATGACAATGCAAAGAAGTTTAT 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTGATAGGAGATAATGACAATGCAAAGAAAGTTTAT 517
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Homo sapiens
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Best Local Similarity 99.8
Matches 557; Conservative
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:966"
/db_zref="taxon:966"
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/clone_lib="WHH MGC 68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Technologies.
                                                                                                                                                                                                                                                                                                                    GAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGAC 515
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Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
                                                                                                                                                                                                                                                                                                                                           11 GAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGGAGAAGAC
                                                                                                                                                                                                                                                                                                                                                                                      TTGCAACAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGATGATTTTTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 ATGATGTCTCGGGAAGAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 CACCATGATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTAGAAAATGAAGGATAGAAATCACAGAAGTAACTGCTCCCCTGAGGATAATCCTGTA
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                                                                                                                                                                                                                                                         Length 868;
                                                                                                                                                                                                                                                    tch 21.1%; Score 491; DB 5; Length 86 al Similarity 100.0%; Pred. No. 8.4e-252; 491; Conservative 0; Mismatches 0; Indels
     Location/Qualifiers
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Homo sapiens
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491 GTACCACCAGA 501
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Eutheria; Dutheria; Primates; Catarrhini; Hominidae; Homo.

E J (bases 1 to 866 c.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contect: Robert Strausberg, Ph.D.

Email: cgapbe-remail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Prasyed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be http://inage.llni.gov
Plate: LibMi3327 row: f column: 07

High quality sequence stop: 667.
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                                                                                                               227
                                                                                                                                        868 bp mRNA linear EST 02-MAY-2002
7574911 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6059910
                                                                                                                                                             GGTTTANGGTGATTGCATGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC 240
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                                               Gaps
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               Length 711;
                                           1; Indels
           Score 493; DB 7; I
Pred. No. 6.8e-253;
0; Mismatches 1;
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       Best Local Similarity 99.8%;
Matches 543; Conservative
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Homo sapiens
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5', mRNA sequence.
BQ232651
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BQ232651
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602692270F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4824712 5', mRNA sequence.
                                                                                                                                                                                                                                                                  /tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="GRN_ES"
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from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
          networks that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAG
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           Transcriptome characterization elucidates signaling control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004) Contact: Brandenberger R
                                                                                                                                                                                                                                                                                                                                                                                                Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                             Regenerative Medicine
Geron Corporation
721 Constitution Drive, Menlo Park, CA 94025, UT 181 650 473 8658
Fax: 650 473 7760
Email: rbrandenbergeregeron.com
Insert Length: 770 Std Error: 0.00.
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ا
                                                                                                                                                                                                                                                                                                                                                                                              Score 461; DB 7; L Pred. No. 1.2e-235; 0; Mismatches 1;
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                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
 Lebkowski, J and Stanton, L.W
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Best Local Similarity 99.8%;
Matches 511; Conservative
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BG720220
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/note="oligo dT_primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
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1 (Dasas I to 770)
1 (Dasas I to 770)
1 Erandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                            mol_type="mRNA"
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/tisque_type="embryonic stem cells, DMSO-treated H9 cell
isoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  611 ACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGACAGTTTCACA
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328775548 GRN_ES Homo sapiens CDNA 5', mRNA sequence.
CN368823
                                                                                                                                                                                                                                                                                                                                                           Length 520;
Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 466

Eax: 650 473 7760

Email: rbrandenberger@geron.com
                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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100.0%; Pred. No. 9.1e-244;
ive 0; Mismatches 0;
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                                                                                                                                                                                     'organism="Homo sapiens"
                                                                                                                        Email: rbrandenberger@geron.com
Insert Length: 520 Std Error:
    Location/Qualifiers
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Homo sapiens
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476; Conservative
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Matches 476,
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CN274513 455 bp mRNA linear EST 16-MAY-2004 17000600026439 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
                            1179 GAGAAGAGGAGAAGTAATGAGGTGCTACGTGGAGCCATCGAGACCTACCAAGAGGTGGCC 1238
421 AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="GRN PREHEP"
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feed DNSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
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1 (bases 1 to 0, 455)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Transcriptom characterization elucidates signaling networks that control human ES cell growth and differentiation
Contact: Brandenberger R.
Regenerative Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAACTCCGTAAAAGGGGAAAATTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACG
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230 Constitution Drive, Menlo Park, CA 94025,
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
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19.6%; Score 455; DB 7; Le
Best Local Similarity 100.0%; Pred. No. 1.8e-232;
Matches 455; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bmail: rbrandenberger@geron.com
Insert Length: 455 Std Error: 0.00.
Location/Qualifiers
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                                                                                     481 AAATGGTACACGCAGAACATGTTGAGGGA 509
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I (bases 1 to 689)

NIH-MGC http://mgc.nci.nih.gov/.

Muthonlished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbe-rémail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CONA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

CONA Library Arrayed by: The I.M.A.G.B. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.B. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be

http://image.llnl.gov

Plate: LLAMI0736 row: k column: 17

High quality sequence stop: 685.

Location/Qualifièrs

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// Clone Ilbe-"NHH MGC 97"

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19.7%; Score 458; DB 4; Length 689;
Best Local Similarity 99.8%; Pred. No. 4.6e-234;
Matches 508; Conservative 0; Mismatches 1; Indels
          sapiens (human)
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/tissue_type="dorsal root ganglia"
/dev stage="adult, 36 yr"
/dev stage="adult, 36 yr"
/lab_host="DH10B"
/lab_host="DH10B"
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/clone_lib="Lupski_dorsal root ganglion"
/clone="Vector: pGWV-SPORT6" (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
Directionally cloned using the following adaptors:
5. TGGACCAGGGTCGCAGGGCGCCCCT(15)-3'. Size selected
5. GACTAGTTCTAGATCGCAGGGGCGCCCCT(15)-3'. Size selected
1 bf for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

2B 1 (Dases 1 to 857)

RS NIH-MGC http://mgc.nci.nih.gov/.

RS NIH-MGC http://mgc.nci.nih.gov/.

AL (Dases 1 to 857)

AL (Dases Forcatail.nih.gov/.

Contact: Robert Strausberg, Ph.D.

Email: Gapbas-remail.nih.gov

Contact: Robert Strausberg, Ph.D.

Email: Gapbas-remail.nih.gov

Contact: Robert Strausberg, Ph.D.

Contaction Robert Strausberg, Ph.D.

Contaction Robert Strausberg, Ph.
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AGENCOURT 8118183 Lupski dorsal root ganglion Homo sapiens CDNA clone IMAGE:6181443 5', mRNA sequence.
                                                                                                                                                                                                              1846 TCCTGCCTGAGGATGAAACCTGAGGGAAAAAGGGACTGGAGCCAGTTCACGCTGTGGC 1905
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                                    375 CACAGCCTTGGTGGACCCCCAAAGAAAGAAGGGCTACACAGAGTTAGTATAGTTTAGAAA
                                                                                                                                     495 rccriccordadcardanaaccreangeanaangegeacresagcongrecorgresses
1726 CACAGCCTTGGTGGACCCCAAAAGAAACGGGCTACACAGAGTTAGTAAAGTCTTTAGAAA
                                                                                                        1786 GAAACTGGAAAGTTAATCCCAGATGAAGGCCTTGCAGTGATGGATAAAGCCAAAGGTCTCT
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Best Local Similarity 99.8%; Pred. No. 9.8e-230;
Matches 500; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/clone="IMAGE:6181443"
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I bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushina-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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Pred. No. 7.6e-231;
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/tissue type="rectum"
/clone_lib="Sugano cDNA library, rectum"
                                                                                                                                                                                                            GCTAAAGTCCATTATGGCTTCATCCTGAAGGCACA 1513
                                                                                                                                                                                                                                     Query Match
19.4%; Score 452; DB
Best Local Similarity 99.6%; Pred. No. 7.6e
Matches 552; Conservative 0; Mismatches
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Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Eutheria; Eutheria; Eutheria; Eutheria; Eutheria; I (bases 1 to 920)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Gapbs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be http://image.llni.gov

Clone distribution: MGC clone distribution information can be http://image.llni.gov

Fluction(dthrough the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 565.

// Organism="Hono sapiens"
// Mo_Lype="mgNN"
// Mo_Lype="mgNN"
// Abex="mala"
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AGENCOURT 8215289 Lupski sympathetic_trunk Homo sapiens CDNA clone
IMAGE:61876655', mRNA sequence.
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                                      AGCATGGAGGACACAAGAATGGGAGGAAAAGGCGGACTCTCGGGGAACTTCATTCTTCACGT
                                                                                                                                           GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH108"
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BQ722578.1 GI:21861475
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/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCTCCG-3' and
5'-ATCATCTRACATCCCGACGCCCCCT(15)-3'. Size selected >
1' SATAGTTCTRACATCCGACGCCCCCT(15)-3'. Size selected >
1' Not for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor Technologies); available through Life
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sapiens cDNA clone IMAGE:5952075
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1014)
NHI-MGC http://mgc.nci.nih.gov/.
NAID-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                CGGACCGTGCAATGCCCAGCGTAAGAATGCCAAGAGCAGCGCCAACAGCAGCAGCAGCA
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Pred. No. 9.9e-230;
0; Mismatches 1; Indels
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AGENCOURT 6910858 NIH_MGC_110 Homo
S', mRNA sequence.
BU190749 GI:22704733
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Best Local Similarity 99.8%;
Matches 500; Conservative 0
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cDNA Library Preparation: Rubin Laboratory

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Location/Qualifiers
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AU132666.1 GI:10993205
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can life and through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov i column: 04
High quality sequence stop: 695.
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                                                                                                                                                                                                                                                            HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y.,
Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T.,
Sugano,S., Masuho,Y., Isogai,T.)
Unpublished (2000)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 767)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3986
Email: genomics@hri.co.jp
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTITGATGIGGATGATGCCAAAGTTTTATTAGGACTTAAAGGAGAGTCTACTTCAGAGC
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                                                                                                                                    Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.
Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y. and
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/db_xref="taxon:9606"

/dloa="NT2P4000310"

/cell type="teratocarcinoma"

/cell_line="NT2"

/dloa="teratocarcinoma"

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/con="teratoca
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/ organiam="Homo sapiens"
/mol_type="manA"
/db xref="taxon.9606"
/dev_stage="Adult"
/door_lib="taxon.9606"
/dev_stage="Adult"
/clone_lib="NN0045"
/note="organ: nervous normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini_library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Dases I to 519)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 518.
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QV2-NN0045-181200-560-d11 NN0045 Homo sapiens CDNA, mRNA sequence.
BF962729
CAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG 900
                                                                                                                                                                                                                                                                         408
                                                                                                                                                                                                                                                                                                                        901 AAGTAAGCATTTTCCTGTGGAAGAACAGCAGGAAGTACCACCAGAAACAAATAGAAAAA 960
                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                               781 ACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCA
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Directionally cloned into EcoR1/Kho1 sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callfornia, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                     BUS502606 911 bp mRNA linear EST 12-SEP-2002 AGENCOURT 10023130 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6480917 5', mRNA sequence.
BUS502606
             Institutes of institutes of institutions of in
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NIH MGC http://mgc.nci.nih.gov/.
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19.2%; Score 447; DB 5; Length 911;
Best Local Similarity 100.0%; Pred. No. 4.1e-228;
Matches 447; Conservative 0; Mismatches 0; Indels
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Homo sapiens
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/do xref="taxon:9606"
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No. 196,716 - ludwig Institute for Cancer Research)
profiles into the BUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
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17000424344521 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
CN368827
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 695)
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Li, Y., Ku, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
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                                                                                                                                                                                                                                                                                                            Length 537;
                                                                                                                                                                                                                                                                                                        18.8%; Score 436; DB 2; Length 53 99.8%; Pred. No. 3.1e-222; ive 0; Mismatches 1; Indels
                                      1. .537
/organism="Homo sapiens"
High quality sequence stop: 533
Location/Qualifiers
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Homo sapiens
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Matches 486; Conservative
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleoștomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 537)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. T., Zago,M.A., Bordin,S., Costa,F.F., Brunstein,A., de Oliveira,F.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., Goliweira,P.S., Bucher,P., Jongeneel,C.V., O', Sares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: +55-11-2707001
mail: abimpoon@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Project. This entry can be seen in the following URL
Project. To this entry can be seen in the following URL
Project. This entry can be seen in the following URL
800-323-f036-323-2000-08-22844=1)
Seq primer: puc 18 forward
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QV2-NN0045-220800-323-f03 NN0045 Homo sapiens CDNA, mRNA sequence.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                           GAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAGGAGAACCACAACAA
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proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
       Length 519;
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         18.8%; Score 438; DB 4; Le
100.0%; Pred. No. 2.5e-223;
ive 0; Mismatches 0;
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                                                 Matches 438; Conservative
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Fisk, G.J.,

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                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 554)
Pouetka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann, S.).

EST (Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and
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                                                                                                                                                                                                                                                                                       This is the 5' sequence of the clone insert Clone from S. Wiendann, Molecular Genome Analysis, Germann Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germann Cancer Research Center, Heidelberg/Germann Cancer Research Center, German Genome Project.

No sl sequence available is available at the RZPD in Berlin. Please contact the RZPD: Ressourcerzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERWANN; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 1. .554 |
| Organism="Homo sapiens" |
| Organism="Homo sapiens" |
| Ab xref="awn 1960s" |
| Ab xref="mrNa" |
| Ab xref="more" |
| Acoust = "more" |
| Acoust = "more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GAGGGTTGGGAACAAAGAGGCATATAAGTGGTATGAGCTTGGGGCACAAGAGAGGACCTT
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99.8%; Pred. No. 2.6e-216;
tive 0; Mismatches 1;
                                                                                                                                                                                                     Wiemann, S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.8<sup>3</sup>
Matches 475; Conservative
                                                                                                                                                                                                                                                Contact: MIPS
                                    Homo sapiens
Homo sapiens
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             KEYWORDS
SOURCE
ORGANISM
                                                                                                                            REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                     JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:900"
/tisue type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN_BB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hBS cell lines
H1 [p23], H7 (p29), and H9 (p26) maintained in feeder-free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL700393 S54 bp mRNA linear EST 04-SEP-2003 DKFZ6686K01118 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686K01119 5', mRNA sequence.
AL700393 GI:19620926
Transcriptome characterization elucidates signaling networks that control human BS cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
Geron Corporation
Tel: 650 473 8658
Fax: 650 473 760
Email: rbrandenbergerageron.com
Insert Length: 695 & Ed Error: 0.00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AGCATGGAGGACACAAGAATGGGAGGAAAGGCGGACTCTGGGGAACTTCATTCTTCAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCAGCAACAGCAGCAGCAGCGG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC 240
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Pred. No. 5.4e-219;
0; Mismatches 1;
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99.8%;
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conditions.
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Best Local Similarity 99.89
Matches 480; Conservative
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540

579

600

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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s wiemann@dkfz- heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 bp mRNA linear EST 04-SEP-2003 DKFZp762H093 r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762H093-5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 GITITATTAGGACITAAAGAGAGAICTACTICAGAGCCAGCAGCAGCCGCCAGAAGAGGGCI 383
                                                                                                                                                                                                                                                                                        Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Denomic from Sequence available.

No B1 Sequence available.

This clone (DKFZp762H093) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenbug, GERWANY; Email: clone@rzpd.de.

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 424)
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehrer, et al.)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 AAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAG
CAGCAGTCCCCGCCAGAAGAGGCTGAGCCACACTGAGCCCGAGGAGCAGGTTCCTGTGG
                        400 CAGCAGTCCCGCCAGAAGAGCTGAGCCACACACACACTGAGCCCGAGAAGCAGGTTCCTGTGG
                                                                                    AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG
                                                                                                                          460 AGGCAGAACCCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG
                                                                                                                                                                                                                                                       541 GAGAACCACAACAAGAGATGATGACTTTCTTATGGCGACTGATGTAGATGATAGATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"
| hab_host="DHIOB"
|/clone lib="762 (synonym: hmel2)"
|/note="Vector: pSportl; Site_1: Notl; Site_2: Sall"
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18.2%; Score 424; DB 1; Length 424;
Best Local Similarity 100.0%; Pred. No. 8.4e-216;
Matches 424; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="melanoma (MeWo cell line)"
                                                                                                                                                                                                                                                                                                                                             601 AGACCCTGGAACCTGAAGTATCTCATGAA 629
                                                                                                                                                                                                                                                                                                                                                                                      640 AGACCCTGGAACCTGAAGTATCTCATGAA 668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp762H093"
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LOCUS
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TITLE
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/db_xref="taxon:9606"
/clone="INABRA"
/lab_host='Mthora (all line"
/tissue type="carcinoma, cell line"
/tolon=lib="NHH MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit-
(Stratagene) and Superscript II T (Life Technologies).
Note: this is a NIH_MGC Library."
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10023079 NIH_MGC_40 Homo sapiens CDNA clone IMAGE:6480842
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 959)
S NIH-MGC http://mgc.nci.nih.gov/.
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CONA Library Preparation: Rubin Laboratory
CONA Library Preparation: Rubin Laboratory
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://mage.llnl.gov
Plate: LLCM2661 row: e column: 03
High quality sequence stop: 591.
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                                                                  5', mRNA sequence.
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carried out using a Not I primer-adapter [5--pgActraGATACGACGACCGCCCC(T(1)2-1/]. CDNA was cloned in Not I/Gal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC),"
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1 (bases I to 5014)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, C.S., Simpson, D.H., Brunstein, A., Gollveira, P.S., Bucher, P., Jongeneel, C.V., Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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QV2-NN0045-041000-403-b08 NN0045 Homo sapiens CDNA, mRNA sequence.
BF943222.1 GI:12360497
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                      CGGACCGTGCAATGGCCCAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGCA
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                                                                                                         Length 606;
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Best Local Similarity 99.8%; Pred. No. 9e-216;
Matches 474; Conservative 0; Mismatches 1
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Homo sapiens
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Fax: +55-11-2707001
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                                                                                                                  503
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                                                                GATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTT
                                                                                                                              181 GATGAGGAAAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTT
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/mol_type="mRNA"
/db_xref=taxon:9606"
/clone=hw08b05"
/cell_type="pericytes"
/dev_stage="Adult"
/lab_host="BMDH108"
/clone_lib="Human primary human ocular pericytes.
/maplified (hw]
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Homo sapiens
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COMMENT
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//note="Correction" is yes; Vector: pSport1; RNA was extracted from primary human pericytes in culture. A directionally cloned primary human pericytes in culture. A directionally cloned cDNA library in the pSPORTI vector [Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protechology (Laurel MD) essentially was carried out using a Not I primer-adapter [5-pactpartTrangarGGGGGGGGCGCCC(T)] essentially was [5-pactpartTrangarGGGGGGGGGCGCCC(T)] essentially was cloned in Not I/Sal I sites. Est analysis was performed at the NIH Intramural Sequencing Center (NISC)."
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UnamplIfied (hw)"
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                      cultured
                                                           pericytes
Unpublished (2004)
Contact: Wistow G
Section on Molecular Structure and Function
                                                                                                                                                           National Eye Institute 6/31, NIH, Betheeda, MD 20892-2740, USA 7E1: 301 402 3452 Fax: 301 496 0078 Email: graeme@helix.nih.gov plate: 08 row: b column: 10 Seq primer: M13RP1 reverse primer (ABI).
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18.2%; Score 423; DB 7; I
Best Local Similarity 99.8%; Pred. No. 3.1e-215;
Matches 473; Conservative 0; Mismatches 1;
                         analysis of
                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="pericytes"
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/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="hw08b10"
Tsal, J.Y. and Wistow, G. Expressed sequence tag
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     AUTHORS
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                                                                                                                                                                                                                            1. .504
/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/dev_stage="Adult"
/clone lib="mN0045"
/note="Organ: nervous normal; Vector: puc18; Site_1: Smal;
/note="Organ: nervous normal; Note="Organ: nervous nervous normal; Note="Organ: nervous nervo
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                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome roject. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-041000-403-b08&t3=2000-10-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 504.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 610)
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Pred. No. 3e-215;
0; Mismatches 1; Indels
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/organism="Homo sapiens"
//organism="MRNA"
//db_xref="taxon:9606"
//dev_stage="Adult"
//dome_lib="Cr0549"
//clone_lib="Cr0549"
//note="Organ: colon; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning_products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, 1 Mamalla, Eutheria; Primates; Catarrhini, Hominidae, Homo. 1 (Dases 1 to 433)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F., Goldman, G. H., Carvalho, A.Fr., Matsukuma, A., Baia, G.S., Simpson, D.H., D'Hare, M.J., Soares, F., Brentani, R., Saias, G. S., Simpson, D.H., Simpson, A., Saias, G. S., Simpson, D.H., Simpson, A., Saias, G. S., Simpson, S., Simpson, S., Simpson, A., Sim
                                                                                                       BQ318605 433 bp mRNA linear EST 17-MAY-2002
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&c2=CM0-CT0549-210900-561-a04&c1=2000-09-21&c4=1)
Seq priner: puo 18 forward 18 forward High quality sequence stop: 413.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539 AGGAGAACCACAAAAAGAGGATGATGAGTTTCTTATGGCGACTGATGTTGATGATGATT 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             479 TGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCAC
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Troc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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418; Conservative 0; Mismatches 0; Indels
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HRI human cDNA project
Upupublished (2000)
Contact: Takao losgai
Genomics Laboratory
Halix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3976
Fax: 81-438-52-3986
Fax: 81-438-52-3986
Fax: 81-408-52-3986
Fax: 81-408
                                                                                 AU138660 AU30EL Homo sapiens cDNA clone FLACE1009036 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                           61 TGAACCTCTAGAAAATGAAGGGATAGAAATCACAGAAGTAACTGCTCCCCCTGAGGATAA 120
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18.1%; Score 420; DB 1; Length 790;
Best Local Similarity 100.0%; Pred. No. 1.3e-213;
Matches 420; Conservative 0; Mismatches 0; Indels
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/ Organism="Homo sapiens"
/ AD_xref="mRNA"
/ Ab_xref="taxon:9606"
/ Clone="PLACE1009036"
/ Lissue_type="placenta"
/ Clone="Tib="PLACE"
/ Clone="Vector: pME18SPL3"
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Homo sapiens
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Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-
181200-563-all&t3=2000-12-18&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 444.
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QV2-NN0045-181200-563-a11 NN0045 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                 295 GAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGAC 354
                                                                                                                                                                                                                                                                                                      576 GCGACTGATGTAGATGATATGAGACCCTGGAACCTGAAGTATCTCATGAAGAAACC 635
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 444)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                   636 GAGCATAGCTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAA 692
                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTAAAGAGAGTCTACTTCAGAGCCAGCAGTCCCGGCAGAAGAGAGGCTGAGCCACACT
                                                                                                                                                               235 GAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGAAAAA
                                                                                                                                                                                                                                                                             ATCTATGATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAAAGTTTTATTAGGA
                                       Arctargargergargargargartrrgargrangargecaaagrrrargaa
                                                                                                          crinanagagarcrinchgagccagcagricccgccagaagaggcrigagccacacac
                                                                                                                                              GAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGCAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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/db_xref="taxon:9606"
/dev_stage="Adult"
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AGENCOURT_6773215 NIH_MGC_128 Homo sapiens CDNA clone IMAGE:5811567
                                                                                                     ATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAAT 838
                                 AGATICCAGIGAACCAGIAGIAGAAGAIGAAAGAITGCACCAIGAIACAGAIGAIGAAC 778
                                                       GACAGITICACAAGACIGIAAICAGGAIAIGGAAGAGAIGAIGICIGAGCAGGAAAAICC 255
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                     839 CACAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTA 896
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http://image.llnl.gov
plate: LLCM2060 row: j column: 16
High quality sequence stop: 394.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
                                                                                                                                                                                                                                                                                                                                                               BQ278505.1 GI:20488713
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Best Local Similarity 100.
Matches 417; Conservative
                                                                                                                                                                                                                                                                                                                               5', mRNA sequence.
BQ278505
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                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                            179
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/lone lib="Human Retina cDNA (Un-normalized, unamplfied): hd/he" (Un-normalized, unamplfied): hd/he" (Done lib="Human Retina cDNA (Un-normalized, norman lib="Human Retina conserved (Norman Eastern Long of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperSoriate Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1628 GAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCACAGAGAGGACACTTTGCATCTGT 1687
                                                                                                                                                                                                                                                                                                                                                                                               primer-adapter
{5'-pGACTAGTTCTAGATCGCGAGCGGCCC(T)15-3'}. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JN368821 740 bp mRNA linear EST 16-MAY-2004
T7000600180518 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
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Homo sapiens
Bukaryota, Metazoa Chordata; Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 740)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Pisk,G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 GAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCACAAGAGAGGAGGACACTTTGCATCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 CTGGGAACGCTCACTCTACAATGTGAATGGACTGAAAGCACAGCCTTGGTGGACCCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1688 CTGGCAACGCTCACTCTACAATGTGAATGGACTGAAAGCACAGCCTTGGTGGACCCCAAA
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                                               /organism="Homo sapiens"
                                                                  Ltype="mRNA"
xref="taxon:9606"
                                                                                                                    /tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMDH10B"
              location/Qualifiers
                                                                                                      /clone="he17b04"
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/clone_lib="NN0045"
/note=-drgan: nervous normal; Vector: puc18; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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1 (Dases 1 to 570)
Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson, K.
Expressed sequence tag analysis of human retina for the NEIBank Project: Rechindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   570 bp mRNA linear EST 15-JUL-2002 cDNA (Un-normalized, unamplified): hd/he hel7b04 5', mRNA sequence.
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                                                                                                                                                                                                                                                       332 AGGACTTAAAGAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGCCACA
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Section on Molecular Structure and Function
National Eye Institute
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Plate: 17 row: b column: 04
Seg primer: M13RP1 reverse primer (ABI).
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Tel: 301 402 3452
Fax: 301 496 0078
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he17b04.yl Human Retina
Homo sapiens CDNA clone
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Fax: 301 496 0078
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                                                                                                                                                                                                                                                                  /tissue_type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7"
/clone_lib="GRN PRENBU"
/note="oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence
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                          Deconversity, and Jean-Cuir...

Jean-Amenty, and Jean-Cuir...

Jean-Amenty of the characterization elucidates signaling networks that control human Es cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine
Geron Corporation

Jon Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 7760

Email: rbrandenberger@geron.com

Insert Length: 740 Std Error: 0.00.
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   Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                  17.3%; Score 402; DB 7; Length 740; 99.8%; Pred. No. 6.4e-204; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
         Li,Y., Xu,C., Fang,R., Gueg]
Lebkowski,J and Stanton,L.W
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Homo sapiens (human)
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Best Local Similarity 99.8
Matches 452; Conservative
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undemiration (1124), Vector: pSport1; RNA was extracted from /note="Organ: Bye; Vector: pSport1; RNA was extracted from primary human pericytes in culture. A directionally cloned primary human pericytes in culture. A directionally cloned constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter (http://www.lifetech.com/). First carried out using a Not I primer-adapter (cond in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC)."
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                                                                                        Tsai,J.Y. and Wistow,G.
Expressed sequence tag analysis of cultured primary human ocular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1105 AAGAACTAGTACGCAAATACCCTCAGAGTCCACGAGCAAGATATGGGAAGGCGCAGTGTG
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/dev_stage="Adult"
/lab_host="EMDH10B"
/clone lib="Human primary human ocular pericytes.
Unamplified (hw)"
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 629)
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                                                                                                                                                                                          Contact: Wistow G
Section on Molecular Structure and Function
National Bye Institute
                                                                                                                                                                                                                                                                     6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                                                                                                                                                                                                                                      Email: graeme@helix.nih.gov
plate: 36 row: h column: 12
Seg primer: M13RP1 reverse primer (ABI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hw36h12"
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Homo sapiens (human)
Homo sapiens

I (bases I to 503)

Jas (baco, B., Garcia (Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., O'Hare, M.J., Soares, F., Brentani, R., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ339559 GV2-NN0045-101100-409-d06 NN0045 Homo sapiens CDNA, mRNA sequence. BQ339559.1 GI:20999368
                                                                                                                                                                                  600 GAGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAG 659
                                                                                                                                                                                                                         Fax: +55-11-2707001
Email: asimpsonobludwig.org.br
This asimpsonobludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/focripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-
101100-409-d06&t5=2000-11-10&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 4.
Location/Qualifiers
377 GAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACA 318
                                                                                                  ACAGITICACAAGACIGIAAICAGGAIAIGGAAGAGAIGAIGICIGAGGAGGAAAAAICCA 719
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Fue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shorgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                           540 GGAGAACCACAACAAGAGGATGATTTCTTATGGCGACTGATGTAGATTTT
                                                                                                                                                                                                                                                                                                                                                GATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGAACA
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brazi]
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// Organism="Homo sapiens"
// Mol_type="mRNA"
// Mol_type="mRNA"
// Mol_type="mRNA"
// Mol_type="mRNA"
// Mole="faxon:9606"
// Clone lib="NN2006"
// Clone lib="NN2006"
// Inote="Organ: nervous normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Indwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Simpson, A.J.

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                            BQ340475 497 bp mRNA linear BST 20-MAY-2002 QV2-NN22006-110501-627-c09 NN2006 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Emall: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN2006-110501-627-c09&t13=2001-05-11&t4=1)
Seq primer: put 18 forward
High quality sequence stop: 496.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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99.6%; Pred. No. 3.5e-200;
ive 0; Mismatches 2;
                                             BQ340475
BQ340475.1 GI:21001375
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BQ340475/c
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Butheria; Primates; Catarrhini; Hominidae; Homo.

B 1 (Dases 1 to 1031)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

L Ontact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

Contact: Robert ATCA/DCTD/DTP

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LLAM13140 row: I column: 08

High quality sequence stop: 425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGENCOURT 7593740 NIH MGC_72 Homo sapiens cDNA clone IMAGE:6065047 5', mRNA Sequence.
BQ223755. GI:20405155
EST.
derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) poffiles into the PUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
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100.0%; Pred. No. 3.5e-200;
ive 0; Mismatches 0;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:605047"
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                                                                                                                        al Similarity 100.
395; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Brunstein,A., deoliveira,P.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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QV2-NN2003-230401-624-a03 NN2003 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_l: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2 kb. Library constructed by Life
Technologies."
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2020263
                                                                                                                                                                                                                  Length 1031;
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                                                                                                                                                                                                                  16.9%; Score 392; DB 5; Le
100.0%; Pred. No. 1.6e-198;
iive 0; Mismatches 0;
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI035330.1 GI:14441956
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Homo sapiens
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/organism="Homo sapiens"
//organism="Homo sapiens"
//organism="mkNn"
//db_xref="taxon:966"
//dev_stage="Adult"
//cone_lib="spr651"
//note="Organ: breast; Vector: puc18; Site_1: Smal; Site_2: Smal; A min:lib=ary was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector: Reverse transcription of tissue mkNA and cDNA amplification were performed under low stringency conditions.
       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 409)
1 (Dases 1 to 409)
1 Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Nagai, M.A., da Cilva, W. Jr., Zago, M.A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Singson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001

Bax: +55-11-2707001

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This sequence was derived from the following URL Project. This entry can be seen in the following URL Project. This entry can be seen in the following URL 6ttp://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PMO-BT0651-150
300-002-go5&t3=2000-03-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 409.
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                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 CCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGAGATGATGTCTGA 43
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                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
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Best Local Similarity 100.0
Matches 385; Conservative
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/ Organiam="Homo sapiens"
// mol_type="mcnn" sapiens"
// mol_type="mcnn" sapiens"
// db_xref="texon:966"
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// note="Organ: nervous normal; Nector: Parkerse research
// note="Organ: nervous normal; Nector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.plrtl=QV2&t2=QV2-NN2O03-230401-624-a03&t3=2001-04-23&t4=1)
Seq primer: put 18 forward
High quality sequence stop: 525.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACCGAGCATAGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGA 691
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGC
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Pred. No. 6e-197;
0; Mismatches 2; Indels
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ilarity 99.6%;
Conservative
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BEO84010/C
LOCUS
DEFINITION
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/tissue_type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7"
/clone lib="GRN PRENBU"
/note="foligo dT_primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 TGAGGAAGTTCTAGGAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGT 310
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Homo sapiens
Homo File Sutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 468)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
In, Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that
Control human Es cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
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318 GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC
                                       241 TIGITGACTATGAGGAAGTICTAGGAAAACTAGGAAICTATGATGCTGATGGTGATGGAG
                                                                CN368831 46-MAY LINEAI EST 16-MAY 1inear EST 16-MAY 17000600846567 GRN_PRENEU Homo sapiens CDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 Constitution Drive, Menlo Park, CA 94025, Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 468 Std Error: 0.00.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Geron Corporation
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/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/lab_host="DH10B"
/clone lib="Lupski dorsal root ganglion"
/clone lib="Lupski dorsal root ganglion"
/clone lib="Uppki dorsal root ganglion"
/clone lib="top".spore"
/college of Medicine) and is available through Life
/college."
                                                                                                                          BU838423
AGENCOURT 8123161 Lupski dorsal root ganglion Homo sapiens CDNA clone IMAGE:6177038 5', mRNA sequence.
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: Dr. James R. Lupski
    Tissue Procurement: Dr. James R. Lupski
    Tissue Progration: Life Technologies, Inc.
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Agencourt Bioscience Corporation
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LLAM13554 row: f column: 15
    High quality sequence start: 66
    High quality sequence stort: 66
    High quality sequence storp: 549.
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1 (Dases 1 to 930)
11 HMGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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16.5%; Score 383; DB.5; L
Best Local Similarity 99.4%; Pred. No. 1.1e-193;
Matches 533; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Organism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9606"
clone="IMAGE:6177038"
           BU838423.1 GI:24022818
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1015 CATCATGCACCCCGGGACTCACGTGTGGCCGCACACAGGGCCCCACAAACTGCAGGCTCCG 2074
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                                                                                                                                                                                                                                                                     EST 16-MAY-2004
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Homo sapiens by sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dasses 1 to 626)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechhol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                       1895 CACGCTGTGGCAGCAAGGAAGAAATGAAAATGCCTGCAAAGGAGCTCCTAAAACCTG
                                                                                                                                                                                                                                                  TACCTTACTAGAAAAGTTCCCCGAGACAACAGGATGCAGAAGAGGACAGATCAAATATTC
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       1996. For additional information, contact:
benco-soares@uiowa.edu
TAG_TISSUBE-Lung Epithelial Cells Tissue nos 359-368
TAG_IB=UI-CP-RN0
TAG_EGGCTGTAGGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CN368826 626 bp mRNA linear EST 16 17000424344515 GRN_EB Homo saplens CDNA 5', mRNA sequence.
                                                                                                                        Length 720;
                                                                                                                    Score 379; DB 6; Length 72
Pred. No. 1.5e-191;
0; Mismatches 1; Indels
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230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 626 Std Error: 0.00.
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                                                                                                               CGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAGGAGAACCACA 550
                                                                                                                                                                             247 CGCAGAACATGTTGAGGGAGAGACTTGCAACAAGAAGATGGACCCACAGAGAGAACCACA 306
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Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
Cwww.openbiosystems.com)
Seq primer: M13 FORWARD
POLYA=Yes.
GGATGATGCCAAAGTTTTATTAGGACTTAAAGAGAGATCTACTTCAGAGCCAGCAGTCCC 126
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1720)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                 CCAGAATATCGAAGGAAGGAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACA
                               GCCAGAAGAGGCTGAGCCACACTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866 Fax: 319 356 7771 Eastle Daul-mccray@ulowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 6 (9), 791-806 (1996)
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CA311352.1 GI:24529450
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Homo sapiens
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/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="embryonic stem cells, embryoid bodies
derived_from H. H7 and H9 cells"

/clone_lib="GRN EB"

/note="oligo dT_prined, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p12), H7 (p29), and H9 (p26) maintained in feeder-free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE876059 1048 bp mRNA linear EST 20-OCT-2000
601485742F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887962 5',
                                                                                                                                                                                                                                                                                                                                                                                                      TIGITGACTATGAGGAAGTICTAGGAAACTAGGAATCTATGATGCTGATGGTGATGGAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTITICATIGITICATICCAAAGTITTATTAGGACTTAAAAGAGATCTACTTCAGAGC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265
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                                                                                                                                                                                                                                                                                                                                            240
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1 (bases 1 to 1048)
NHH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                             1 CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGCG
                                                                                                                                                                                                                                GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC
                                                                                                                                                                                   Gaps
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0
                                                                                                                                                     Length 626;
                                                                                                                                                                                   1; Indels
                                                                                                                                                       Score 370; DB 7;
Pred. No. 1e-186;
0; Mismatches 1;
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BE876059
BE876059.1 GI:10324835
                                                                                                                                                          15.9%;
99.8%;
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Homo sapiens
                                                                                                                 conditions.
                                                                                                                                                                                      Conservative
                                                                                                                                                                         Similarity
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Best Local Si
Matches 420;
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ORGANISM
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AUTHORS
TITLE
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KEYWORDS
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                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3887962"
/tissue_type="large cell_carcinoma, undifferentiated"
/lab_hogt="pH10B (ghage-resistant)"
/clone_lib="NHH MGC 69"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
/ref="Organ: lung; Vector: pCMV-SPORT6; Site_1: Oligo dT.
/ref="Organ: lung; Vector: pCMV-SPORT6; Site_1: Oligo dT.
/ref="Organ: lung; Vector: lung; Vect
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Mooce,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. washU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GCTCCGGCAGCGGTAGCACGGCGGCAGCAGCAGCCCCGGGGCCCCGGAGAGACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 329; DB 2; Length 10
Pred. No. 1.3e-164;
0; Mismatches 2; Indels
11
   Plate: LLAM9667 row: d column:
                               High quality sequence stop: 670 Location/Qualifiers
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Best Local Similarity 99.5%;
Matches 429; Conservative
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/mol_type="mRNN"
/db_xref="taxon:9606"
/tbsuc_type="mbryonic stem cell, retinoic acid and mitogen-treated hES cell line H7"
/clone_lib="GRN_PRENEU"
/clone_lib="GRN_PRENEU"
/note="cligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
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                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 391)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J. and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 GATGCTGATGCTGATGGAGATTTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 GGAACTICATICTICACGIGGITIAIGGIGATIGCAITIGCIGGGCGICTICGACAICIGIA
                            17000600014160 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
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llarity 100.0%; Pred. No. 5.4e-162;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                               Regenerative Medicine
Geron Corporation
720 Constitution Drive, Menlo Park, CA 721 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 393 Std Error: 0.00.
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/organism="Homo sapiens"
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                                             CN368818
CN368818.1 GI:47368752
                                                                                                             Homo sapiens (human)
Homo sapiens
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324;
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Best Local S:
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VERSION
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CN481268
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AL Unpublished (1997)

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810

Email: estewatson, wustl.edu
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@inage.lln1.gov) for further information.
Seq primer: 400P from diboo.
Seq primer: 514 515 1800
Second Consortium (info@inage.lln1.gov) for further information.
Seq primer: 400P from diboo.
Seq primer: 515 1800
Second Consortium (info@inage.lln1.gov) for further information.
Seq primer: 515 1800
Second Consortium (info@inage.lln1.gov) for further information.
Second Consortium Second 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear EST 16-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAIGCIGAIGGIGAIGGAGAITITIGAIGIGGAIGAIGCCAAAGITITAITAGGACITAAA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 GATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402 GAGGAGCAGGTTCCTGTGGAGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAAAA 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 GGAACTICATTCTTCACGTGGTTATGGTGATTGCATTGCTGGGCGTGTGGACATCTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 14.1%; Score 328; DB 1; Length 57. al Similarity 100.0%; Pred. No. 4.1e-164; 328; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
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Best Local S
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Ingolstraedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; Sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                       AL694159
DKFZp313D1441 rl 313 (synonym: hlcc2) Homo sapiens cDNA clone
DKFZp313D1441 s', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 TAATCCTGTAGAAGATTCACAGGTAATTGTAGAAGAAGTAATATTTCCTGTGGAAGA 300
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1 (bases 1 to 527)
Koehrer,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.
EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hlcc2)"
Site_1: SfiIA; Site_2: SfiIB;
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6, 14059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             746 TGAAAGATTGCACCATGATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626 TGAAGAAACCGAGCATAGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGA
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No s1 sequence available.

This clone (DKFZp313D1441) is available at the RZPD in I Please contact the RZPD: Ressourcenzentrum, Heubnerweg (Belase contact the RZPD: Ressourcenzentrum, Leubnerweg (Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.8%; Score 321; DB 1;. Le 100.0%; Pred. No. 2.3e-160; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="DKRZp3131441"
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/note="Vector: pripilEx2; s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.527
/organism="Homo sapiens"
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515 CAGCAGTCCCGCC 527
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Matches 321; Conserv
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                                                                                                                                                                                 ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: Eye; Vector: pSportl; RNA was extracted from primary human pericytes in culture. A directionally cloned cDNA library in the pSPORTI vector [Invitrogen) was constructed at Bloserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter (5.-pdacTaGATGCTAGATCGCAGAGCGCCCC(7)15-3'). cDNA was cloned in Not I //sal I sites. EST analysis was performed the NIH Intramural Sequencing Center (NISC)."
                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                       1 (bases 1 to 580)
Tsai,J.Y. and Wistow,G.
Expressed sequence tag analysis of cultured primary human ocular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC
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/clone lib="Human primary human ocular pericytes.
Unamplified (hw)"
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                                                                                                                                                                                                                            Section on Molecular Structure and Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.9%; Score 322; DB 7; L
|larity 99.7%; Pred. No. 6.9e-161;
| Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                  Tex: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 05 row: d column: 04
Seg primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                                                               National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                                                                                                                                                                                                                                                                                          1...580
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/db_xref="taxon:9606"
/clone="hw05d04"
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                                   Homo sapiens (human)
                                                                                                                                                                           pericytes
Unpublished (2004)
                                                                                                                                                                                                              Contact: Wistow G
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Matches 372; Conserv
                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 1 (Dases I to 484)

13 Ebett,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,

14 Radelof,U., Schneider,D. and Korn,B.

15 Human Uniqueseset - RZPD3

16 Unpublished (2003)

17 Contact: Ina Rolfs

18 RZPD Deutesches Resourcenzentrum fuer Genomforschung GmbH

18 RZPDD INAGOSPSTORASSOURCENZENTRUM (Der Gelection)

18 RZPDI INAGOSPSTORASSOURCENZENTRUM (Der Gollection)

18 RZPDI INAGOSPSTORASSOURCENZENTRUM (Der Gollection)

18 RZPDI INAGOSPSTORASSOURCENZENTRUM (Der Gelection)

18 RZPDI INAGOSPSTORASSOURCENZENTRUM fuer Genomforschung GmbH

18 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

18 RZPD GilonesonschlibNo-972 Contact: Ina Rolfs

19 30 32639 101

10 RZR + 49 30 32639 101

10 RZR + 49 30 32639 101

11 RZPD GilonesonschlibNo-972 Contact: Ina Rolfs

18 RZPD GilonesonschlibNo-972 Contact: Ina RZPD;

19 Contact RZPD GilonesonschlibNo-972 Contact: Ina RZPD;

10 RZR + 49 30 32639 101

11 RZR + 49 30 32639 101

12 RZR + 49 30 32639 101

13 RZR + 49 30 32639 101

14 RZR + 49 30 32639 101

15 RZR + 49 30 32639 101

16 RZR + 49 30 32639 101

17 RZR + 49 30 32639 101

18 RZR 
                                                                                                                                                                                     BX111251 484 bp mRNA linear EST 07-FEB-2003 BX111251 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGP998F034597; IMAGE:1876994, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             907
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 484)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     848 AACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAGAAGTAAG
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                                                                                                                                                                                                                                                                                                                                            BX111251.1 GI:27878432
                                                                                                                                                                                                                                                                                                                                                                              EST.
Homo sapiens (human)
1244 ATTTCCC 1250
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                                                                                                       RESULT 63
BX111251
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
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                                                                                                           2023 bp DNA linear GSS 16-DEC-2003 Pan troglodytes ASPH gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGCCTAAACTTTTAAATAAATTTGATAAGACTATTAAAGCTGAACTTGATGCTGCAGA 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAACTCCGTAAAAAGGGGGAAAAATTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACG 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           944 AAAACTCCGTAAAAAGGGGAAAATTGAGGAAGCAGTGAATGCGTTTAAAGAACTAGTACG 1003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAGAAGAGAGAAGTAATGAGGTGCTACGTGGAGCCATCGAGACCTACCAAGAGGTGGC 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1064 TGAGAAGAGGAGAAGTAATGAGGTGCTACGAGAGCCATCGAGACCTACCAAGAGGTGGC 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGCCTACCTGATGTCCCTGCAGACCTGCTGAAGCTGAGGTTTGAAGCGTCGCTCAGACAG 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1298 GCAACAATTICTAGGICATATGAGAGGITCCCTGCTTACCCTGCAGAGATTAGTICAACT 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1184 GCAACAATTTCTAGGTCATATGAGAGGTTCCCTGCTTACCTGCAGAGATTAGTTCAACT 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           943
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. (bases 1 to 2023) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Nang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission Submission Submission Celera Genomics, 45 West Gude Drive, Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 2023)
Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanebaum, D.M., Givello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 302 (5652), 1960-1963 (2003)
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes (chimpanzee)
                                                                                                                                                                                                                                                                                            AY405268.1 GI:39761242
                                                                                                                                                                                                                                                                                                                                                                                                        Pan troglodytes
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                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                            RESULT 62
AY405268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                 ACCESSION
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KEYWORDS
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/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                 1027 AGACTATTAAAGCTGAACTTGATGCTGCAGAAAACTCCGTAAAAGGGGAAAAATTGAGG 1086
                                                                                                                                                                                                                                                                                                                                                                        1087 AAGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAGCAAGAT 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1147 ATGGGAAGGCGCAGTGTGAGGATGATTTGGCTGAGAAGAGGAGAAGTAATGAGGTGCTAC 1206
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 682)
SS NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                       179 AGACTATTAAAGCTGAACTTGATGCTGCAGAAAACTCCGTAAAAGGGGGAAAAATTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 GIGGAGCCATCGAGACTACCAAGAGGTGGNCAGCCTACCTGATGTCCCTGCAGACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                              239 AAGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGGAGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1267 IGAAGCTGAGTITGAAGCGTCGCTCAGACAGGCAACAATITCTAGGTCATATGA 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 TGAAGCTGAGTTTGAAGCGTCGCTCAGACAGGCAACAATTTCTAGGTCATAG 472
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Location/Qualifiers
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Condinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
761: 319 335 9256
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Louis Staudt
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
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                                                                                                                                                                                                                                                                 1088 AGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAGCAAGATA 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              907 GCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCACCAGAAACAAATAGAAAAAAAGATG 966
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 503)
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Normalization and subtraction: two approaches to facilitate gene
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Best Local Similarity 99.5
Matches 412; Conservative
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CF136513
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DKFZD4681163_r1 468 (synonym: phrtl) Pongo pygmaeus cDNA clone DKFSD4681163_5', mRNA sequence. CR559422 GI:50298874 EST 4.5UL-2004 EST.
                                                                             GGAATCTATGATGCTGATGGTGATTTTTGATGTGGATGATGCCAAAGTTTTATTA 332
                                                                                                                                                       GGACTTAAAGAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGCCACAC 392
                                                                                                                                                                                                                                 AAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAA 512
                                                                                                                                                                                                                                                                                                                                                                      This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagan (Hilden/Germany) within the CDNA sequencing consortium of the German Genome Project. This clone (DKFZp4681163) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact Rzpp for ordering:

http://www.rzpd.de/cgl-bin/products/cl.cgi?cloneiD=DKFZp4681163 http://www.rzpd.de/cgl-bin/products/cl.cgi?cloneiD=DKFZp4681163 available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="rousy prymacus"
/mol_type="mixNa" |
/db_xref="taxon:9600"
/clone="DkF2p4681163" |
/tisne="pkF2p4681163" |
/dev_stage="adult" |
/dev_stage="adult" |
/lab_host="DH108" |
/clone_lib="468 (synonym: phrt1)" |
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                                                            393 ACTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGCA
                                                                                                                                                                                                                                                                                                      ACATCTGTAGCTGTCGTTTGGTTTGATCTTGACTATGAGGAAGTTCTAGGAAAACTA
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Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Forgo pygmaeus mkNa (Bahr, A., Lauber, J., Mewes, H.W., et al.)
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                              513 GACTTGCAACAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGA 562
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Pongo pygmaeus (orangutan)
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                                                             213
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CR559422
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DKFZp4691163 r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
DKEZp4691163 5', mRNA sequence.
                    749
                                                                                                                                         407
                                                                                                                                                                                                              810 GAACCTCTAGAAAATGAAGGATAGAAATCACAGAAGTAACTGCTCCCCTGAGGATAAT 869
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                                                                                                                                                                                                                                                         527
                                                                                                                                                                                                                                                                                                          This is the 5' sequence of the clone insert clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKPZ); Email s.wiemann@dkfz-heidelberg de; sequenced by Qiagen (Hilden/Germanny) within the CDNA sequencing consortium of the German Genome Project. This clone (DKFZp4691163) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:

http://www.rzpd.de/gi.bin/products/cl.cgi?Clone1D=DKFZp4691163

Further information about the clone and the sequencing project is available at http://mips.gf.de/projects/cdna/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pongo pygmaeus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pongo.

1 (Dases 1 to 719)

Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Pongo pygmaeus mRNA (Bahr,A., Lauber,J., Mewes,H.W., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
GAAACCGAGCATAGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATG
                                                                   690 GAAGAAGATGATGTCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGAAGATGAA
                                                                                          870 CCTGTAGAAGATTCACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAGAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 719
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db xref="taxon:9600"
/clone="DkFZp4691163"
/tissue_type="kidney"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
/lab_host="DH10B"
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Pongo pygmaene
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Length 737; Score 308; DB 7; I Pred. No. 2.5e-153; 13.3%; Query Match Best Local Similarity

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 548)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 7760

Email: rbrandenberger@geron.com

Insert Length: 548 Std Error: 0.00.
plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/).First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGTTCTAGATCGCGAGCGCCC(T)15-3']. CDNA was cloned in Not IJSal i sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC)."
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17000424344539 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
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llarity 99.7%; Pred. No. 2.8e-152;
Conservative 0; Mismatches 1;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 560)
Tsai,Jr. and Wistow,G.
Expressed sequence tag analysis of cultured primary human ocular
                                                                                                                                                                                            213 ACATCTGTAGCTGTCGTTTGGTTTGATCTTGACTATGAGGAAGTTCTAGGAAAACTA
                                                                                                                                                                                                                                              Acerciciadecreticerriegricaricaricaricardadaactraragaaaacta
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Email: grame@lelix.nih.gov
Plate: 22 row: f column: 04
Seq primer: MI3RPI reverse primer (ABI).
Seq primer: MI3RPI reverse primer (ABI).

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| colonelitiers | 
                                                                                  GGACTCTCGGGAACTTCATTCTTCACGTGGTTTATGGTGATTGCATTGCTGGGCGTCTGG
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Section on Molecular Structure and Function
National Eye Institute
6/311, NIH, Bethesda, MD 20892-2740, USA
TTE1: 301 402 3452
Fax: 301 496 0078
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Unpublished (2004)
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B. 1 (bases 1 to 52)

E. Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and ZiC Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Ecoun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +182-42-860-4470

Fax: +182-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2219 GATATTCATCGTGGATGTGTGGCATCCGGAACTGACACCACAGAGCAGAGCAGCCATCC 2278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM785890 536 bp mRNA linear EST 05-MAR-2002
K-EST0064453 S9SNU601 Homo sapiens cDNA clone S9SNU601-34-C04 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / tissue_type="Ascites"
/cell_type="Epithelial"
/cell_tine="SNU-601"
/lab_host=="Topip""
/clone_lib="S9SNU601"
/note="Organ: Stomach; Vector: pME18-FL3; Site_1: Xho1;
                                                                                                                                                                                                                                                                                                                     61 GTGGCCGCACAGGCCCACAAACTGCAGGCTCCGAATGCACCTGGGCTTGGTGGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                      2039 GIGGCCGCACACAGGGCCCACAAACTGCAGGCTCCGAATGCACCTGGGCTTGGTGATTCC
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          Average insert size 1.4 kb. Library prepared by Technologies."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S9SNU601-34-C04"
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99.7%;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mathoral Institutes of Health, Mammalian Gene Collection (MGC)
Mathoral Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: capabbe-remail.inh.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arzayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Gond distribution: MGC Clone distribution information can be
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 447.
Location/Qualifiers
from embryoid body outgrowths derived from hES cell lines
HI (p32), HT (p29), and H9 (p26) maintained in feeder-free
conditions."
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                                                                                                                                                                                                                                 381 GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC 440
                                                                                                                                                                                                                                                                                                GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441 TIGTIGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGGTGATGGTGATGGAGGA 500
                                                                                                                                                                                                       CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGCG 60
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//db_xef="taxon:900"
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//nobe="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                  Gaps
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                                                                                                                   Length 548;
                                                                                                                                                             1; Indels
                                                                                                        Query Match
12.8%; Score 297; DB 7; L
Best Local Similarity 99.7%; Pred. No. 1.9e-147;
Matches 347; Conservative 0; Mismatches 1;
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Site 2: Xhol; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including Sit site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using Sfil oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with Sfil and cloned into DraIII - digested pMR185-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coll TOplOF, by electroporation method. The cDNA libraries constructed by this method are full-length enriched CDNA library."
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Song, H., Peng, Y., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Zhang, Q., Han, Z., Chen, Z., Hu, R. and Chen, J. Lu, G., Ye, M., Lu, G., Han, Z., Chen, Z., Hu, R. and Chen, J. Contact: Qinghua Zhang Contact: Qinghua Zhang Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045 (ex. 663332)
Email: mbshidms.shron
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AV751514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 AAAGATTGCACCATGATACAGATGATGTAACATACCAAGTCTATGAGGAACAAG
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351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                        12.7%; Score 294; DB 4; Length 536; 100.0%; Pred. No. 8e-146;
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Best Local Similarity 100.
Matches 294; Conservative
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ENGANCES METEZOA; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 862)

RS MIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Genomics

National Cancer Tastitute / NIH

Bldg. 31 RmloA07 Bethesda, MD 20892

Emall: Gapube-rémail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratorium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDCM195 row: a column: 02

High quality sequence stop: 564.

High quality sequence stop: 564.
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                                                                                      /clone lib="NPD"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
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AGENCOURT 14354806 NIH MGC_186 Homo sapiens cDNA clone IMAGE:30406369 5', mRNA sequence.
                                                                                                                                                                                                                                Length 622;
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| Abb host="DH10B (T1 phage-resistant)"
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                                                                                                                                                                                                                                Query Match 12.7%; Score 294; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 8.2e-146;
Matches 294; Conservative 0; Mismatches 0;
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/clone="IMAGE:5540329"

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Bribaria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Bribaria; Butheria; Bribaria; Bribaria; Bribaria; Homo.

S NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Nuthonal Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapabs-remail.nih.gov

Charary Preparation; Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLAMI2236 row: e column: 02

High quality sequence stop: 579.
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12.7%; Score 294; DB 6; Length 862;
Best Local Similarity 100.0%; Pred. No. 8.7e-146;
Matches 294; Conservative 0; Mismatches 0; Indels
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/tissue_type="melanotic melanoma"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2 kb. Library constructed by Life
Technologies."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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al Similarity 99.5%; Pred No. 1.5e-142;
388; Conservative 0; Mismatches 2; Indels
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230 Constitution Drive, Menlo Park, CA 94025, USA
716: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 767 Std Error: 0.00.
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derived_from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
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from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
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Search completed: March 25, 2005, 22:28:27 Job time : 6796 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: March 25, 2005, 14:29:03; Search time 1157 Seconds (without alignments) 11890.647 Million cell updates/sec	Title: US-09-436-184-3 Perfect score: 2324 Sequence: 1 cggaccgtgcaatggcccagcttgggaaactctggagaga 2324	Scoring table: OLIGO NUC Gapext 60.0	Searched: 4390206 seqs, 2959870667 residues	Word size : 0	umber of hits sa	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Listing first 100 summaries	Database : N Geneseg 16Dec04:*	1: genesequisous: 2: genesequisous:*	3: genesequi2000s:* 4: genesequi2001as:* 5: genesequi201as:*	6: genesequ2002as:* 7: genesequ2002bs:*		10: geneseqn2003cs:* 11: geneseqn2003ds:*		No. is the number of results predicted by chance to	to the score of the of the total score d	SUMMARIES	Result Query No Score March Langeth DB ID	A 40rc 0 001 40rc	2324 100.0 2324 8 ABS57868	2222 295.6 2452 13 ADP23914	2171 93.4 5358 10 2171 93.4 5358 10	895 38.5 2680 6 ABAU41/8 895 38.5 2680 13 ADP24208	640 27.5 2442 2 AAZ23609 640 27.5 2442 6 ARK19743	640 27.5 2442 8 ACA12072	640 27.5 2442 8 ACA03258 640 27.5 2442 10 ADH47310	640 27.5 2442 13 ADJ21229 615 26 5 3110 11 ACM89788	502 21.6 2048 10 ACA92448 502 21.6 2048 0 ACA92448	ACA4/ ABQ59507 Abq59 ADT94758 Adt9	104 4.5 161 12 ACH93769 Ach93769 Human

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The invention relates to diagnosing a neoplasm and inhibiting tumour growth in a mammal, using an antibody that binds to human separtyl growth in a mammal, using an antibody that binds to human separtyl contacting a tissue with a detectably-labelled antibody where an increase in level of antibody binding at tissue site compared to the level of binding to normal non-neoplastic tissue indicates the presence of a neoplasm at the tissue site. Inhibiting tumour growth in mammal involves administering the antibody conjugated to a cytotoxic agent to a mammal. Also included are a method of conferring an immune response to a tumour cell in a mammal, by administering the antibody, a method of inducing an HAAH-specific immune response in a mammal, by daministering the mammal an HAAH polypeptide (or a polynuclectide composition encoding the polypeptide, or its degenerate variant), a fragment of HAAH comprising an
                                                                                                                                                                                                                                                                                           Human; se; gene; aspartyl (asparaginyl) beta-hydoxylase; HAAH; cytostatic; immunostimulant; antibody; neoplasm; tumour; PB50; 86A; 5C7; 19B; brain tumour; glioma; glioblastoma; astrocytoma; haemangioma; pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer; liver cancer; cancer of the bile ducts; primary malignant CNS neoplasm; metastatic CNS neoplasm.
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    Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue mammal with detectably-labeled antibody which binds to human aspartyl (asparaginyl) beta-hydroxylase.
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(DMON/) DE LA MONTE S M.
(DEUT/) DEUTCH A H.
(GHAN/) GHANBARI H A.
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cc antibody or its fragment which binds to HAAH (where the antibody is FB50, antibody or its fragment which binds to HAAH (where the antibody is FB50, CC 57 or 19B), a hybridoma cell line chosen from hybridoma FB50, HA386A, HA15CA and HA219B, and a fragment of HAAH which lacks enzymatic activity or alpha-ketoglutarate binding domain and epidermal growth cactivity or alpha-ketoglutarate binding domain and epidermal growth in a mammal, conferring an immune cr mammal, inhibiting tumour growth in a mammal, conferring an immune creaponse to a brain tumour cell (e.g. glioma, glioblastoma, astrocytoma or haemangioma) in a mammal, for conferring immune response in a mammal. The method is useful for diagnosing malignant creaplasms derived from endodermal tissue, e.g. colon cancer, breast cancer, pancreatic cancer, liver cancer and cancer of the bile ducts. The method is also useful for diagnosing neoplasms of central nervous system (CNS) e.g. primary malignant CNS neoplasms of both neuronal and glial cumours e.g. glioma, glioblastoma, and for diagnosing brain tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma. The concert sequence encodes human HAAH astrocytoma or haemangioma.
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λά	721	AITCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGTAGAGAT 7	08 6
අු	721	ATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATACAGATGAAGATTCCAGATGAACAT	0 9
δλ	781	accaagtctatgaggaacaagcagtatatgaacctctagaaaatgaagggatagaaatta 8	0 40
QQ	781	ACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAA1UA 8	0 4.
λ	841	841 CAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG 900	006
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οy	901	AAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCACCAGAAACAAATAGAAAA 9	096
qa	901	aagtaagcattititccigiggaagaacaggaagtaccacagaaacaaatagaaaaa 9	096
ολ	961	CAGATGATCCAGAACAAAAGCAAAAGTTAAGAAAAAGAGCCTAAACTTTTAAATAAA	1020
QQ	196	CAGATGATCCAGAACAAAAGCAAAAGTTAAGAAAAAGAAGGAGCCTAAAACTTTTAAATAAA	1020
οy	1021	TTGATAAGACTATTAAAGCTGAACTTGATGCTGCAGAAAAACTCCGTAAAAGGGGAAAAA 1	1080
Db	1021	TTGATAAGACTATTAAAGCTGAACTTGATGCTGCAGAAAACTCCGTAAAAGGGGAAAAA	1080
λŏ	1081	TTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAG 1	1140
Dp	1081	TTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAG	1140
٥'n	1141	CAAGATATGGGAAGGGGGGGTGTGTGAGATGATTTGGCTGAGAAGAGGGGAAGTAATGAGG	1200
QQ	1141	CAAGATATGGGAAGGCGCAGTGTGAGATGATTTGGCTGAGAAGAGGAGAAGTAATGAGG	1200
Οy	1201	TGCTACGTGGAGCCATCGAGACCTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGCAG	1260
Db	1201	TECTACGIGGAGCCATCGAGACCTACCAAGAGGIGGCCAGCCTACCIGATGTCCCTGCAG	1260
ογ	1261	ACCIGCIGAAGCIGAGIITIGAAGCGICGCICAGACAGCCAACAAITICIAGGICATAIGA	1320
qq	1261	accigcigaagcigagitigaagcgicgcicagacaagcaatticiaggicataa	1320
Oy	1321	GAGGTTCCCTGCTTACCCTGCAGAGATTAGTTCAACTATTTCCCAATGATACTTCCTTAA	1380
qq.	1321	GAGGITCCCTGCTTACCCTGCAGAGATTAGTTCAACTATTTCCCAATGATACTTCCTTAA	1380
٥٧	1381	AAAATGACCTTGGCGTGGGATACCTCTTGATAGGAGATAAGAAAGGAAAGGTTT	1440
ΩÞ	1381	APAATGACCTTGGCGTGGGATACCTCTTGATAGGAGATAATGACAATGCAAAGAAAG	1440
ζ	1441	ATGAAGAGGTGCTGAGTGACACCTAATGATGGCTTTGCTAAAGTCCATTATGGCTTCA	1500
Db	1441	AIGAAGAGGIGCIGAGIGIGACACCIAAIGAIGGCITIGCIAAAGICCAITAIGGCIICA	1500
٥٧	1501	TCCTGAAGGCACAGAACAAAATTGCTGAGAGCATCCCATATTTAAAGGAAGG	1560
QQ	1501	TCCTGAAGGCACAGAACAAAATTGCTGAGAGCATCCCATATTTAAAGGAAGG	1560
٥٧	1561	CCGGAGATCCTGGCACTGATGATGGGAGATTTATTTCCACCTGGGGGATGCCATGCAGA	1620
qq	1561	CCGGAGATCCTGGCACTGATGATGGGAGATTTTATTTCCACCTGGGGGATGCCATGCAGA	1620
λ̈́	1621	GGGTTGGGAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCACAAGAGAGAG	1680
QQ	1621	GGGTTGGGAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCACAAGAGAGGACACTTTG	1680
δý	1681	CATCTGTCTGGCAACGCTCACTCTACAATGTGAATGGACTGAAAGCACAGCCTTGGTGGA	1740
QQ	1681	CATCTGTCTGGCAACGCTCTACAATGTGAATGGACTGAAAGCACAGCCTTGGTGGA	1740
٥٨	1741	CCCCAAAAGAAACGGGCTACACAGAGTTAGTAAAGTCTTTAGAAAGAA	1800
Dp	1741	CCCCAAAAGAAACGGGCTACACAGAGTTAGTAAAGGTCTTTAGAAAGAA	1800
٥٧	1801	TCCGAGATGAAGGCCTTGCAGTGATGATAAAGCCAAAGGTCTCTTCCTGCCTG	1860

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                                                                                                                                                                                   The present invention relates to a method for inhibiting tumour growth is a mammal. The method comprises administering to the mammal a compound, which inhibits the expression or enzymatic activity of a human aspartyl (asparaginyl) beta-hydroxylase (HAAH). The compound may inhibit HAAH hydroxylation of a NOTCH polypeptide. In particular, the compound may inhibit hydroxylation of an epidermal growth factor (EGF)-like repeat sequence in a NOTCH polypeptide. The methods are useful for inhibiting tumour growth or killing tumour cells, or for diagnosing or neoplasm is colon cancer. Deace, pancreatic cancer inhibiting cancer, breast cancer cancer of the bile ducts, or cancer or tumour of the central nervous system (CNS). The present sequence encodes HAAH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GCTCCGGCAGCGGTAGCACGAGTGCGGCAGCAGCAGCCCCGGGGCCCCGGAGAGAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAG
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                                                                         Inhibiting tumor growth or killing tumor cells (e.g. cancer of the cobreast, pancreatic, liver or the central nervous system), by administering an inhibitor of the human aspartyl (asparaginyl) beta-
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ive 0; Mismatches
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Ince
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Matches 2324; Conservative C
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Wands JR,
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                                                                                                                                                                                                                                                                                                                                                                                       Tumour growth inhibition; human aspartyl (asparaginyl) beta-hydroxylase; HAAH hydroxylation; NOTCH polypeptide; epidermal growth factor-like repeat; EGF-like repeat; tumour cell; malignant neoplasm; colon cancer; breast cancer; pancreatic cancer; liver cancer; cancer of the bile duct; cancer the central nervous system; CNS; cytostatic; gene; ss; human.
                                                                                                                                                                                                                                                                                                  CAACAGGATGCAGAAGAAGAACAAATATTCCATCATGCACCCCGGGACTCACGTGT
                                                                                                                                                                                                                                                      TCATCTTTGATGACTCCTTTGAGCACGAGGTATGCCAGGATGCCTCATCTTTCCGGCTGA
                                          AAAACCTGAGGGAAAAAGGGGACTGGAGCCAGTTCACGCTGTGGCAGCAAGGAAGAA
                                                                                                        ATGAAAATGCCTGCAAAGGAGCTCCTAAAACCTGTACCTTACTAGAAAAGTTCCCCGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding human aspartyl (asparaginyl) beta-hydroxylase (HAAH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
12. .2288
/*tag= a
/product= "HAAH"
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(DMON/) DE LA MONTE S M.
(INCE/) INCE N.
(CARL/) CARLSON R I.
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AA WPI; 2004-419628/39.		Dp
Schoenfe	1621 GGGTTGGGAACAAAGAGCGTATAAGTGGTATGAGCTTGGGCACAAGAGAGGACACTTTG 1680 1681 CATCTGTCTGGCAACGCTCACTATGTGAATGTGAATGGACTGAAAGCACACGCTTGGTGGA 1740	원 장
PR 01-NOV-2002; 2002US-0423394P. XX XX	621 GGGTTGGGAACAAAGAGCATTATATATATATATATATAGCTTGGCACAAGAGAACATTTG 168	3 8
30-OCT-2003; 2003WO-US03431	1561 CCGGAGATCTGGCACTGATGATGAGAATTTTATTTCCACCTGGGGATGCCATGCAGA 1620	<u>ک</u> ۾
PN W02004041170-A2. XX PD 21-MAY-2004.		연
Unidentified	501 TCCTGAAGGCACAGAACAAAATTGCTGAGAGCATCCCATATTTAAAGGAAGG	6
	1441 ATGAAGAGCTCTGAGTGTGACACCTAATGATGCTTTGCTAAAGTCCATTATGGCTTCA 1500 	δ q
KW ss, gene, PRO, antiinflammatory, antiarthritic, antir KW immunosuppressive, osteopathic, antidiabetic, dermato	AAAATGACCTTGGGGTGGGGTACCTCTTGATGGGGGTAATGACAATGCAAAGATTT 1	qq
AA DAY PEPTING ENCODING CDNA SEQ ID NO:1092.	1381 AAAATGACCTTGGCGTGGGATACCTCTTGATAGGAGATAATGACAATGCAAAGAAAG	δ
AC ADP23914; XX DT 18-NOV-2004 (first entry)	1321 GAGGITCCCIGCTIACCCIGCAGAGAITAGITCAACTATITCCCAAIGAIACTICCITAA 1380 	දු දු
RESULT 4 ADP23914 ID ADP23914 standard; cDNA; 2452 BP. XX	1261 ACCTGCTGAAGCTGAGTTTGAAGCGTCGCTCAGACAACAATTTCTAGGTCATATGA 1320 	දු පු
	1201 TGCTACGTGGAGCCATCGAGACCTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGCAG 1260 	දුරු පු
Db 2221 TATTCATCGTGGATGTGTGGCATCCGGAACTGACACCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	1141 CAAGATATGGGAAGGCGCAGTGTGAGGATGATTTGGCTGAGAAGAGAGAAGTAATGAGG 1200 	දු දු
2161	1081 TTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCTCAGAGTCCACGAG 1140 	දු පු
2101	1021 TTGATAAGACTATTAAAGCTGAACTTGATGCTGCAGAAAAACTCCGTAAAAGGGGAAAAA 1080 	Sp Sy
	961 CAGATGATCCAGAACAAAAGCAAAGTTAAGAAAAAGAAGCCTAAACTTTTAAATAAA	දු පු
1981	901 AAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCACCAGAAACAAATAGAAAA 960 	දු දු
1921	841 CAGAAGTAACTGCTCCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG 900 	දු දු
1861	781 ACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCA 840 	상 임
1801	721 ATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATAGATGATGTAACAT 780 	8 &
Db 1741 CCCCAAAAGAAACGGGCTACACAGAGTTAGTAAAGTCTTTAGAA OV 1801 TCCGAGATGAAGGCCTTGCAGTGATGAAGGCCAAAGGTCTC	661 CAGITICACAAGACTGIAATCAGGATATGGAAGAGATGATGTGAGCAGGAAAATCCAG 720 	g g
Qy 1741 CCCCAAAAGAAACGGGCTACACAGAGTTAGTAAAGTCTTTAGAA	rggaacctgaagtatctcatgaagaaaccgagcatagttaccacgtggaagaga 66	QQ

ragaaagttccccgaga 1980 ||||||||||||||||| |agaaagttccccgaga 1980 CCTCATCTTTCCGGCTGA 2220 AGAGACGCAGCCTTCCAG 2280 ACCCCGGGACTCACGTGT 2040 ACCCCGGGACTCACGTGT 2040 irheumatic; tological; ropic; respiratory; PM, Wood WI;

The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiarinflammatory, antiarinflammatory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its of the invention may have a use in gene therapy. The PRO polypeptide, its polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, inventile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Siparen's syndrome, systemic classes, a demoslinating disease of the central or peripheral nervous crowscultis, sarcoidosis, autoimmune haemolytic anaemic autoimmune chronic active hepatitis, primary disease, infectious or autoimmune chronic active hepatitis, primary disease, infectious or autoimmune chronic active hepatitis, primary disease, infectious or autoimmune chronic active hepatitis, primary disease, an autoimmune or immune-ensitive neteropathy, Mnipple's disease, arthma, allergic minutes, sclerosing chilary cirrhosis, granulomatous hepatitis, sclerosing chilary cirrhosis, primary disease, erythema multiforme, contact dermatitis, sociasis, an allergic disease, a bullous skin disease, erythema multiforme, contact dermatitis, psociasis, an allergic hypersensitivity, urticaria, an immune or immune-organicated disease, a bullous or contact disease, activity, urticaria, an immune organicated disease, graft rejection or contact disease, gr New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system. Claim 1; SEQ ID NO 1092; 2940pp; English P-PSDB; ADP23915

Sequence 2452 BP; 779 A; 507 C; 657 G; 509 T; 0 U; 0 Other;

121 AGCATGGAGGACACAAGAATGGGAGGAAAAGGCGGACTCTCGGGAACTTCATTCTTCACGT 180 246 240 306 300 ATTITGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAGAGAGATCTACTTCAGAGC 360 CAGCAGTCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCCGAGGAGCAGGTTCCTGTGG 420 CAGCAGTCCCCCCAGAAGAGGCTGAGCCACACACTGAGCCCGAGGGGGGGTTCCTGTGG 486 AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG 480 1 CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGCG 60 GGTTTATGCTGATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTTGATC GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC TTGTTGACTATGAGGAAGTTCTAGGAAACTAGGAATCTATGATGCTGATGGTGATGGAG 0; Gaps DB 13; Length 2452; Query Match · 95.6%; Score 2222; DB 13; Length 2 Best Local Similarity 99.9%; Pred. No. 0; Matches 2322; Conservative 0; Mismatches 2; Indels 61 127 181 247 241 307 367 361 427 421 301 g Š q ò g 8 g 중 음 g a ઠે ò ò

QQ	487 AC	AGSCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG 546
ο̈́λ	481 A	SGTACACGCAGAACATGTTGAGGGAGAAGACCTTGCAACAAGAAGATGGACCCACAG
qq	547 A	AAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCCACAG 606
ò	541 G	CTTATGGCGACTGATGTAGATGATAGATTTG 60
qq	607 G	
λο i	- A	GACCCTGGAACTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGA 660
Q C	7	,
ò	н	CAGTITCACAAGACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAATCCAG 720
qq	727 C	7
ò	721 A7	7
Д	787 AT	CAGTGAACCAGTAGTAGAAGATGAAGATTGCACCATGATACAGATGATGTAACAT 8
ò	81 A	CCAAGTCTATGAGGAACAAGGAGTATATGAACCTCTAGAAATGAAGGATAGAATCA 840
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qq	1327 AC	recreaacreacrireaacerecereaacaacaacaarrreragrearara
ò	1321 GA	GAGGITCCCTGCITACCCTGCAGAGATAGTTCAACTATTTCCCAATGATACTTCCTTAA 1380
qq	-	-
ò	1381 AA	-
qq	1447 AA	AAATGACCTTGGCGTGGGATACCTCTTGATAGGAGATAATGACAATGCAAAGAAAG
ογ	1441 AT	-
QQ	1507 AT	ATGAAGAGTGCTGAGTGTGACCTAATGATGGCTTTGCTAAAGTCCATTATGGCTTCA 1566
ò	1501 TC	CCTGAAGGCACAGAAATTGCTGAGAGCATCCCATATTTAAAGGAAGG
Dp	1567 TC	cigaaggcacagaacaaaiigcigagagcaicccaiaiiiaaaggaagg

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Hayes

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Identifying an agent that modulates the function of an apoptosis-associated polypeptide, useful for diagnosing or treating e.g. cancer, comprises comparing the binding of the polypeptide to the candidate agent
                                                                                                                                                                                                            claim 2; SEQ ID NO 55; 304pp; English.
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                                                                                         Keating
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                                                                    (EIRX-) EIRX THERAPEUTICS LTD
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P-PSDB; ADR97348.
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                           CAACAGGATGCAGAAGGACAGATCAAATATTCCATGCACCCCGGGACTCACGTGT
            CCGGAGATCCTGGCACTGATGATGGGAGATTTTATTTCCACCTGGGGGATGCCATGCAGA
                                                                                                                                                      gene; ds; human; apoptosis; cancer; inflammation; autoimmune; neurodegenerative disorder; cytostatic; antiinflammatory; immunosuppressive; neuroprotective; gene therapy; ASPH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAATTTAGCATGAATTCATGCAAGCTTGGGAAACTCTGGAGAGA 2390
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This invention relates to novel agents that modulates the function of human apoptosis-associated proteins specified within the specification. Specifically, it refers to a method for the identification of target of genes whose expression is correlated with an early stage in the regulation of apoptosis. The present invention describes a method of contacting either candidate agents or control agents to the target genes and assessing the difference of binding and inhibitory activity, where the candidate agent is selected from a low molecular weight organic molecule, an antibody or fragment thereof, an antisense oligonucleotide, a small inhibitory daRNA, or a ribozyme. As such, the compositions and tecthods are useful for diagnosing and treating diseases or conditions associated with abnormal apoptosis in mammalian tissue, such as cancer, inflammation, autoimmune or neurodegenerative disorders. Accordingly, than exhibit cytostatic, antiinflammatory, immunosuppressive and neuroprotective activities. These may also be used for drug screening there are associated with the regulation of apoptosis that can be considered by the compositions are associated with the regulation of apoptosis that can be
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                                   AAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAG
                       AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG
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                                                                                                                                                                                                                                                                   This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to expressed in MYCN activated cells. Specifically, it refers to polynucleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a protococate that is amplified in neuroblastoma cells and is common in small cell lung cancers. The present invention describes these cDNA molecules as useful for in hybridisation assays to detect expression of nucleic as useful for in hybridisation assays to detect expression of nucleic cells of complementary nucleic acids) in a present in a given sample, as useful for complementary nucleic acids) in a present in a given sample, so pecifically bind the cDNA as a ligand and modulate function or activity specifically bind the cDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polynucleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTHS: This sequence does not appear in the printed specification but has been obtained in electronic format from the USP patent Office at
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                                                                                                                                                                                          New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
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larity 99.9%; Pred. No. 0;
Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 63; 27pp; English.
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                                                                   23-FEB-2001; 2001US-0270784P
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                                                                                        (STUA/) STUART S G.
(NUCH/) NUCHTERN J G.
(PLON/) PLON S E.
(SHOH/) SHOHET J M.
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Matches 2321; Conserv
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The invention relates to new isolated nucleic acid molecule comprising a nucleic acid molecule consisting of a gene differentially expressed in cells undergoing differentiation from mesenchymal cell to a chondroblastic phenotype, or hybridiaing under stringent conditions to them for their fragments. Also included are expression vectors, to the induce differentiation of a mesenchymal cell and may be used as an immunogen ), binding partners of the polypeptides, a method for edentifying an agent useful in modulating mesenchymal cell and induction activity of a molecule, a method for a nucleic acid molecule or its expression product, a method for determining regression, progression or onset of cartilaginous tissue degeneration condition in a condition or onset of cartilaginous tissue degeneration condition in a cubject characterised by aberrant expression of a nucleic acid molecule or its expression product, a method for treating a cartilaginous tissue degeneration condition, a method for treating a cartilaginous tissue degeneration condition developing in the cubject, an emethod for treating a cartilaginous tissue degeneration condition and a solid-phase nucleic acid molecule array consisting essentially of a set of nucleic acid molecule array consisting essentially of a set of nucleic acid molecule array consisting essentially of a set of nucleic acid molecule as cited above (or known from known genes shown to be condition, and agents and agents at useful for treating cartilaginous tissue degeneration and infference analysis, RDA), its expression products or fragments, fixed to a solid substrate. The nucleic acids, polypeptides and agents are useful for treating cartilaginous tissue degeneration and as observables and agents are useful for treating cartilaginous tissue degeneration and as observables and agents are useful for treating cartilaginous conditions such as solid substrate. The nucleic acid degeneration conditions when as osteroarchinitis, the mucleic acid cubic arthritis, adjuvant arthritis defenments 
                                                                                                                                                                                                                                                                 New nucleic acid molecules capable of promoting chondrogenesis, useful for diagnoshing and treating cartilaginous tissue degeneration conditions, e.g. osteoarthritis, rheumatoid arthritis, gout arthritis, or osterochondrosis.
antiinflammatory; representational difference analysis
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                                                                                                                                                                           (BGHM ) BRIGHAM & WOMENS HOSPITAL INC
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ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                          PRO polypeptide encoding cDNA SEQ ID NO:1386.
                       ADP24208 standard; cDNA; 2680
                                                                                                                                                                                                     WO2004041170-A2
                                                                                                                                                                               Unidentified
                                                                       18-NOV-2004
                                              ADP24208,
RESULT 8
ADP24208
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GCTCCGGCAGCGGTAGCACGAGTGCGGGCAGCAGCAGCCCCGGGGGCCCGGAGAGACAA AGCATGGAGGACACAAGAATGGGAGGAAAAGGCGGACTCTCGGGGAACTTCATTCTTCACGT GGTTTATGGTGATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC

CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGCAGC

CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGCAGCA

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Score 895, DB 13; Length 2680; Pred. No. 0; 0; Mismatches 1; Indels 0;

38.5%; 99.9%;

Matches 945; Conservative

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121 121

61 61

Similarity

Query Match Local 241

21-MAY-2004

181 241

181

TTGTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAAG

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The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antinflammatory, antiaarthritic, antinflammatory, antiaarthritic, antiallergic, antiaarthmatic, hepatotropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its of the invention may have a use in gene therapy. The PRO polypeptide, its systemic upus erythematosus, rheumatoid arthritis, osteoarthritis, osteoarthritis, sarcoidosis, autoimmune related disorder such as systemic inflammatory myopathy, Sjogren's syndrome, systemic consolitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thromborytopenia, thyroiditis, diabetes mellitus, immune-mediated renal cisease, ademyelinating polyneuropathy, systemic system, idiopathic demyelinating polyneuropathy, a hepatopiliary cirrhosis, granulomatous hepatitis, socionable consoliary cirrhosis, granulomatous hepatitis, socionable consoliary, urticaria, an immune-mediated skin disease, asthma, allergic rhintis, atopic dermatitis, decorasis, an allergic chinitis, atopic dermatitis, contact dermatitis, contact dermatitis, contact dermatitis, pooriasis, an allergic rhintis, atopic dermatitis, contact contact dermatitis, contact dermatitis, contact dermatitis, atopic dermatitis, contact dermatitis, and protection or contect dermatical c
                                                                                                                                                                                                                                                                                                                               New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
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                                                                                                                                                                            PM,
                                                                                                                                                                            Williams
                                                                                                                                                                               Van Lookeren M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             claim 1; SEQ ID NO 1386; 2940pp; English
                   30-OCT-2003; 2003WO-US034312
                                                                        01-NOV-2002; 2002US-0423394P
                                                                                                                                                                               Schoenfeld J,
                                                                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                               WPI; 2004-419628/39
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                                                                                                                                                                                  Clark H,
Wu TD;
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This invention describes a novel polymucleotide and polypeptide sequence for the antigen detected by the antibody MCA 44-3A6. This antigen is designated Labyrinthin (Lab). Antibodies directed to the Labyrinthin and Labyrinthin (Lab). Antibodies directed to the Labyrinthin (Lab) protein are useful for the detection of Lab. The Lab protein is useful in diagnostic assays for cancer, e.g. to monitor the presence and amount of antibodies (this method is especially useful for cancer cells that have the Lab marker). As the Lab gene is not tissue-specific, it will detect cancer regardless of which organ it occurs in. Peptides cancers and/or to treat humans with cancer. Antibody MCA 44-3A6 is able to differentiate antigen associated with adenocarcinomas. However, the sequence of the antigen detected by this antibody as not been elucidated in the prior art. Determination of the polypeptide and polymucleotide sequence of this antigen would enhance its usefulness in cancer diagnosis, treatment and prevention. The present invention discloses the sequence of the antigen recognized by the MCA 44-3A6 antibody. This sequence concodes the human lab protein described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 GGAACTICATICTICACGIGGTIAIGGTGATIGCATIGCIGGGGGTCIGGGACATCTGIA 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                          27.5%; Score 640; DB 2; Length 24:
99.9%; Pred. No. 6.5e-287;
ive 0; Mismatches 1; Indels
                                                                                                Novel Labyrinthin polynucleotides and polypeptides used marker for cancer and in anticancer vaccines.
                                                                                                                                        Claim 1; Fig 1; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 99.9
hes 690; Conservative
          (RADO/) RADOSEVICH J A.
                                                            WPI; 1999-580307/49.
                                                                          P-PSDB; AAY33642
                                    Radosevich JA;
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70. .837
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/product= "lab"
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                             GATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA
                                                                                                                                                                                                                                                                       cDNA encoding clone #48005 (L979P) of lung tumour protein version #2
                                                                                                                                                                                                                                                                                                Lung tumour; cancer; T cell; immune response stimulator; cytostatic;
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                                                                                                             AATGAAGGGATAGAAATCACAGAAGTAACTG 852
                                                                                                                             Claim 7; SEQ ID NO 1791; 223pp; English
                                                                                                                                                                                                     ABK39743 standard; cDNA; 2442 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUL-2000; 2000US-00614124.
29-AUG-2000; 2000US-00651853.
08-SEP-2000; 2000US-00671325.
06-OCT-2000; 2000US-00671325.
30-OCT-2000; 2000US-0077419.
13-DEC-2000; 2000US-007765.
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                                                                                                                                                                                                                                                     (first entry)
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Marnerakis M,
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DB 6; Length 2442;

27.5%; Score 640;

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                                 162 GGAACTTCATTCTTCACGTGGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTA
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expansion; CD4; CD8.
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Pred. No. 6.5e-287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a polymuclectide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences mentioned in complement of S1, sequences (S2) mentioned in specification, complement of S1, sequences consisting of at least 20 contiguous residues complement of S1, sequences consisting of at least 20 contiguous residues CC of S1, sequences that hybridise to S1, sequences having 37$, preferably CC of S1, sequences mentioned in the specification, a sequence consisting the polymental sequences mentioned in the specification, a sequence concomplement of S1, or degenerate variants of S1. Also included are an isolated polymerleotide, or sequences having at least 70$, or expression vector comprising the polymerleotide operably linked to an expression control sequence, a host cell transformed or transfected with the vector, an isolated antibody (or its antigen-binding fragment) that specifically binds to the polymerleotide, detecting the presence of a cancer of a patient, a fusion protein comprising the polymerleotide, protein conditions, stimulating and/or expanding treals specific for a tumour conditions, stimulating and/or expanding the polymerleotide, protein or antigen protein (comprising cells, under conditions and for a time sufficient or antigen-presenting cells, under conditions and for a time sufficient conditions and/or expanding the prolymucleotide, protein or a patient with the polymucleotide, protein or a patient with the polymucleotide, protein or a patient with the polymucleotide, protein or prolymerleotide, protein and scells and the inhibiting the presenting cells and thus inhibiting the development of a cancer in a patient (particularly lung cancer in a patient polymucleotide is also lung in the des
                                                                                                                                                                                                                                                                                                                                                                                                                          Novel lung cancer polynucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides and profess in tumour cells. An amplified portion of the polynucleotide is useful for isolating a full-length gene from a suitable library. The present sequence is a cDNA (full length, extended or partial) isolated from a library derived from lung tumour/cancer cells. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO at seqdata.uspto.gov/sequence.html?DocId=20020197669
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13-DEC-2000; 2000US-00736457.
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Matches 690; Conservative
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                                             BANGUR C S.
FANGER G R.
WANG A.
WANG T.
SWITZER A P.
MCNEILL P D.
CLAPPER J D.
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P-PSDB; ABU69516.
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Clapper JD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            706 AATGAAGGATAGAAATCACAGAAGTAACTG 736.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00416492.
99US-00419356.
99US-00466867.
99US-0046687.
200US-00519642.
200UUS-00533077.
200UUS-00546259.
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17-DEC-1999;
30-DEC-1999;
06-MAR-2000;
22-MAR-2000;
10-APR-2000;
27-APR-2000;
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The invention relates to novel compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer. The compositions comprise one or more lung tumour polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cells that express such polypeptides, and T cells that are specific for cells expressing such polypeptides. The novel compositions have cytostatic and immunostimulant activity. The lung tumour antigens can be used in the creation of a vaccine. The polynucleotides that encode the lung tumour polypeptides can be used in gene therapy to help in the treatment of lung tumoure. This polynucleotide sequence represents a human lung tumour cDNA clone of the invention. This sequence was not shown in the specification. It has been taken from a World Intellectual Property Organization CD ROM supplied with the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 GCTGTCGTTTGGTTTGATCTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTAT 281
                                                                                                                                                                                                                                                                                                                                                            lung cancer; tumour; cytostatic; immunostimulant; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAACTTCATTCTTCACGTGGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vedvick TS;
                                                   586 TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCAT
                                   GATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptides and encoding polynucleotides, useful for diagnosing, preventing and/or treating lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2442;
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Fanger GR,
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Pred. No. 6.5e-287;
0; Mismatches 1;
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Ο,
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                                                                                                                         706 AATGAAGGATAGAAATCACAGAAGTAACTG 736
                                                                                                                                                                                                                                                                                                                             Human lung tumour cDNA clone, SEQ ID No 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kalos P
Carter D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watanabe Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-OCT-2002; 2002WO-US034777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-OCT-2001; 2001US-00017754
28-MAR-2002; 2002US-00113872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson JC, Retter MV
Bangur CS, Mcnabb A;
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                                                                                                                                                                                                                                                                                                                                                                                      human; clone; ss.
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                                                                                                                                                                                                                                                                                                                                                                                 The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polynucleotide associated with the compositions and methods for the therapy and diagnosis of lung cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGATGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                    composition for treating
                                                                                                                                                                                                                                    Mcnabb
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0
                                                                                                                                                                                                                Y, Johnson JC, Retter MW;
Vedvick TS, Bangur CS, MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2442 BP; 781 A; 391 C; 512 G; 758 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                        cancer
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Local Similarity 99.9%; Pred. No. 6.5e-287;
nes 690; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                      New polynucleotide, useful for preparing a c
inhibiting development of cancer, e.g. lung
                                                                                                                                                                                                                                                                                                                                                        Example 5; SEQID NO 1791; 82pp; English.
                                                                                                                                                                                                                      Watanabe
                                                                                                                                                                                                                                    GR,
              05-JUN-2000; 2000US-00589184.
11-JUL-2000; 2000US-00614124.
29-AUG-2000; 2000US-00651563.
08-SEP-2000; 2000US-006588124.
26-SEP-2000; 2000US-006713125.
06-CCT-2000; 2000US-00677419.
30-CCT-2000; 2000US-00702705.
13-DEC-2000; 2000US-00702705.
                                                                                                                                                                                                                                    Fanger
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                                                                                                                                                                                                                      Wang T
                                                                                                                                                                                                                                                                        WPI; 2003-328427/31
                                                                                                                                                                                      (CORI-) CORIXA CORP
                                                                                                                                                                                                                      Henderson RA, Wan
Durham M, Carter
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The invention relates to a novel isolated polynucleotide comprising a sequence chosen from any one of 40 lung tumour polypeptides or its complements, fragments or degenerate variants. The method of the invention has cytostatic applications and may be useful for detecting and treating lung cancer in a patient, as well as for inhibiting the cells isolated from a patient with at least one component chosen from a polypeptide, polynucleotide or antigen presenting cell (APC) of the polypeptide, polypucleotide or antigen presenting cell (APC) of the invention and administering an effective amount of the proliferated T cells to the patient. The current sequence is that of the human lung cancer-related GDNA of the invention. The current sequence is not shown in the specification per se but is available on the USPTO web-site http:seqdata.uspto.gov/sequence.html?DocID=20030211510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTCAGTCCCTTCTCCATGAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAA 521
                                                                                                                                                                                                                         Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 GGAACTTCATTCTTCACGTGGTTTATGGTGATTGCTGGGCGTCTGGACATCTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGTCGTTTGGTTTGATCTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTAT
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                                                                                                                                                                                                                                                                                                                 Novel polynucleotide encoding lung tumor polypeptides, useful diagnosing, preventing and treating cancer e.g. lung cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2442 BP; 781 A; 391 C; 512 G; 758 T; 0 U; 0 Other;
                                                                                                                                                                                                            Sleath PR;
Fanger GR,
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Ο,
                                                                                                                                                                                                            Watanabe Y, Kalos
Durham M, Carter
                                                                                                                                                                                                                                                                                                                                                              Example 5; SEQ ID NO 1791; 99pp; English.
11-JUL-2000; 2000US-00614124.
29-AUG-2000; 2000US-00651563.
26-SEP-2000; 2000US-00658124.
26-SEP-2000; 2000US-00671325.
06-CCT-2000; 2000US-00677419.
30-CCT-2000; 2000US-00702705.
13-DEC-2000; 2000US-00945647.
03-MAY-2001; 2001US-0094541.
29-CCT-2001; 2001US-000113872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 99.9 es 690; Conservative
                                                                                                                                                                                                          Henderson RA, Wang T,
Johnson JC, Retter MW,
Bangur CS, Mcnabb A;
                                                                                                                                                                                                                                                                     WPI; 2004-167010/16.
P-PSDB; ADJ21244.
                                                                                                                                                                               (CORI-) CORIXA CORP.
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GATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAAAGTTTTATTATTAGGACTTAAA
                                                                                                                       GAGGAGCAGGTTCCTGTGGAGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAA
                                                                                                                                                                                                                                          ATTCAGTCCCTTCTCCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGAAGACTTGCAA
                                                                                                                                                                                                                                                                                   GATGCTGATGGTGAGATTTTGATGTGGATGATGCCCAAAGTTTTATTAGGACTTAAAA
                                                                                                      GAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCC
                                                                                                                                                                                                                         ATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAA
                                                                                                                                                                                                                                                                                                                                              GATGTAGATGATAGATTTTGAGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                         AGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lung tumour; cytostatic; lung cancer; human; ss; L979P; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human lung cancer-related extended L979P cDNA - SEQ ID 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGAAGGGATAGAAATCACAGAAGTAACTG 852
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99US-00419356.
99US-00476300.
2000US-00519642.
2000US-00519642.
2000US-0054642.
2000US-00546259.
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17-DEC-1999;
06-MAR-2000;
22-MAR-2000;
10-APR-2000;
27-APR-2000;
27-APR-2000;
27-APR-2000;
05-JUN-2000;
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15-OCT-1999;
17-DEC-1999;
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THE SECTION OF SECTION

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Mismatches

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Matches

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The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for electecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful a marker for breast cancer and in breast cancer therapy, Sequences given
                                                                                                                                                                                                                               705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web
                              525
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641
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                             GATGTAGATGATAGATTTGAGACCCTGGAACTTGAAGTATCTCATGAAGAAACCGAGCAT
                                                               AGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGATGTG
                                                                                              AGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGATGATG
                                                                                                                                TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGAAGATGAAAGATTGCACCAT
                                                                                                                                                                 TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCAT
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                                                                                                                                                                                                                               GATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA
GATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated polypeptide associated with breast cancer, useful fo
detecting presence of polypeptide in sample, as a marker for breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3110 BP; 1039 A; 488 C; 618 G; 915 T; 0 U; 50 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at segdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 9938; 36pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer related marker,
                                                                                                                                                                                                                                                                                                                                                                                 ACN88788 standard; DNA; 3110
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Length 3110;

26.5%; Score 615; DB 11; I 100.0%; Pred. No. 2.8e-275;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATGGCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAGA
                                                                                                                                                                                                                                                                                        895 AACCGAGCATAGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGA
                                                                                                                                                                                                                                                                                                                                         955 AGAGATGATGTCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTAGAAGATTCACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAGAACAGCA
                                                   CACTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGC
                                                                                                       AAAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGA
                                                                                                                     TATGGCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAGA
                                                                                                                                                                                                                                                               632 AACCGAGCATAGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGA
                                                                                                                                                                                                                                                                                                                  AGAGATGATGTCTGAGGAGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAG
                                                                                                                                                                                                                                                                                                                                                                    ATTGCACCATGATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGA
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 AGGACTTAAAGAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGGCTGAGCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACA92448 standard; DNA; 2648 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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ACA92448
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDMs dequences, appearing as ACH12789-ACH50813, whose sequence was determined by the technique of 58H (sequencing by hybridiaation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleac and sequences care useful in diagnostics as axpressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent dat one form part of the printed specification, but was cobtained in electronic format directly from USPPTO at sequence. Hall proceed the 2804 isolated cDNA/EST sequences.
                                                                                                                                                                                  Human, 88; sequencing by hybridisation, SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
479 ATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAA 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                 CAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGATGAGTTTCTTATGGCGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 34279; 44pp; English.
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STACHE-CRAIN B
DICKSON M C.
JONES L W.
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(STAC/)
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(JONE/)
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modification and maintenance molecules (PWMM), and the polymucleoride
sequences encoding them. A total of 40 PMMM polypeptides (designated PMMM
- 1 to PMMM-40) are disclosed. The sequences of the invention are useful
for disgnosing a condition or disease associated with the expression of
for disgnosing a condition or disease associated with the expression of
pMMM in a subject, preparing a polycloan or monocloan antibody, and
generating an expression profile of a sample containing the
pMMM in a subject, preparing a polycloan or monocloan antibody, and
polymucleotides. The diseases or conditions associated with decreased
colored coldes. The diseases or conditions associated with decreased
polymucleotides or the diseases or conditions associated with decreased
colored colored colored colored colored disorders (e.g. epilopsy,
luntington's disease, stroke), immune/inflammatory disorders, (e.g. ADDS,
allergies), developmental disorders (e.g. hypothyroidism, Cushing's
syndrome), agarrointestinal or epithelial disorders, and infections. The
PMMM polypeptides or their fragments are useful in screening compounds
for effectiveness as agonists or antagonists of the polypeptides, or in
altering the expression of the target polymucleotide and compounds that
colored colore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, atherosclerosis, or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAA 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGCAAAAGAACAAA 461
                                                                                                                                                                                                                                                           Emerling BM, Yang J, Lee SY,
EA, Griffin JA, Li JX,
Lehr-Mason PM, Kable AE, Yue
Tang TY, Jin P, Chlen D;
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Pred. No. 1e-222;
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                                                                                                                                                                                                                                                                                   Tran UK, Becha SD, Duggan BM, Lee EA, G
Sprague WW, Hafalia AJA, Chawla NK, Lehr
Marquis W, Yao MG, Richardson TW, Tang
Bhatia U, Burrill JD, Lee S, Blake JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 306; 311pp; English.
            12-OCT-2001; 2001US-0329689P.
25-OCT-2001; 2001US-0335703P.
09-NOV-2001; 2001US-034887P.
28-NOV-2001; 2001US-0334145P.
06-DEC-2001; 2001US-0337451P.
14-DEC-2001; 2001US-034084P.
                                                                                                                                                                                                        (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                        Gorvad AE,
                                                                                                                                                                                                                                                                                                                                                                                                                      2003-430274/40.
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P-PSDB; ABU92053.
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Best Local Si
Matches 502;
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Claim 1; Fig 1; 796pp; English
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                                                                                     AAGGCGCAGTGTGAGGATGATTTGGCTGAGAAGAGGAGAAGTAATGAGGTGCTACGTGGA 1211
                                                                                                                                                                                                                               GCCATCGAGACCTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGCAGACCTGCTGAAG 1271
                                                                                                                                                                                                                                                                 CTGAGTTTGAAGCGTCGCTCAGACAGGCAACAATTTCTAGGTCATATGAGAGGTTCCCTG 1331
                                                                                                                                                          GTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAGCAAGATATGGG 1151
                                                                                                                                                                                                             343
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                                                                                                                                                                                                                                                                                 463
                                                    912 TITCCIGIGGAAGAACAGCAGGAAGIACCACCAGAAACAAAIAGAAAAAACAGAIGATCCA 971
                                                                164 ATTAAAGCTGAACTTGATGCTGCAGAAAACTCCGTAAAAGGGGGAAAATTGAGGAAGCA 223
                                                                                                                                                                    or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell tissue type, and in antisense therapy.
                                                                                                                                                                                                                                         284 AAGGCGCAGTGTGAGGATGATTTGGCTGAGAAGAGGAGAAGTAATGAGGTGCTACGTGGA
                                                                                                                        ATTAAAGCTGAACTTGATGCTGCAGAAAAACTCCGTAAAAAGGGGAAAAATTGAGGAAAGCA
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                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  Human colon cancer related nucleotide sequence SEQ ID NO:3202.
                   Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; colon cancer; cancer; tissue profiling; forensic; m
genetic analysis; diagnostic; antisense therapy; gene; ss.
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 BP; 178 A; 97 C; 119 G; 106 T; 0 U; 2 Other;
                                  0; Indels
                                                                                                                                                                                                                                                                                                    CTTACCCTGCAGAGATTAGTTCAACTATTTCCCAATGAT 1370
                                                                                                                                                                                                                                                                                                              CTTACCCTGCAGAGATTAGTTCAACTATTTCCCAATGAT 502
                 19.8%; Score 459; DB 9; 100.0%; Pred. No. 1e-202;
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                                   0; Mismatches
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Thiaglingam A, Lewis ME;
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                                                                                                                                                                                                                                                                                                                                                                ABQ59507 standard; cDNA; 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-2001; 2001WO-US030732
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                   Matches 459; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FARB ) BAYER CORP.
                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
  Sequence 502
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                   Query Match
Best Local
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ABQ59507/
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AB056306 to AB060787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the AB060776 to AB060787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample of coll cancer in a cell or tissue type, for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate or accorrange on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GICTGAGCAGGAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGA 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S; humoral immune response; cellular immune response; cytostatic; immunostimulant; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TICACAGGIAATIGIAGAAGAAGIAAGCATITITICCIGIGGAAGAACAGCAGGAAGIAC 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  581 TGATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  641 TAGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAAATTGCACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.4%; Score 359; DB 6; Le 100.0%; Pred. No. 3.4e-156;
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Matches 359; Conservative
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The invention relates to polynucleotide and polypeptide sequences

associated with cancer, particularly colon cancer. Also disclosed are (i)

can expression vector comprising the polynucleotide, (ii) an isolated

transformed or transfected with the expression vector, (iii) an isolated

cantibody, or its antigen-binding fragment, which specifically binds to

cancer in a patient, (v) a fusion protein comprising at least one of

the polypeptides, (vi) an oligonucleotide that hybridises to the

cc of cancer in a patient, (v) a fusion protein comprising at least one of

the polypeptides, (vi) an oligonucleotide that hybridises to the

cc of cancer in the polypeptide sequence under highly stringent conditions, and (vii) a

method of stimulating and/or expanding T cells specific for a tumour

cc of c6448, C6358, C6378, C6408, C6358 or one of the potential open reading

cc frames (ORPS) of C6358. These polypeptides are encoded by the

cc polynucleotide sequences, where both are capable of eliciting a humoral

and/or cellular immune response. The polynucleotides, polypeptides are useful for diagnosing, preventing or transing cancer,

cc particularly colon cancer. The polynucleotide and polypeptide success

cc particularly colon cancer. The polynucleotide and polypeptide success

cc particularly colon cancer. The polynucleotide and polypeptide success

cc analysis, nucleic acid purification, isolation of transcriptionally

cantive genes, blocking or transcription factor binding, genome cleavage

cc in situ hybridisation, and as enhancers of transcription or

cc biomarkers. This sequence data for this patent was obciained in electronic

connact directly from the USPPTO web site at seqdata.uspto.gov
                                                                                                                                                                                                                                                                                            New isolated nucleic acids and polypeptides capable of eliciting humoral and/or cellular immune response, useful for diagnosing, preventing or treating cancer, particularly colon cancer.
                                                                                                                                                                                 Secrist
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                                                                                                                                                                           Lodes MJ,
Stolk JA;
                                                                                                                                                                              Indirias CY,
, Durham M,
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 277; 87pp; English.
                                                                                                                                                                           Xu J, Inc
Smith CL,
07-FEB-2001; 2001US-0267382P.
11-MAY-2001; 2001US-0290322P.
12-UUJ-2001; 2001US-0305265P.
16-AUG-2001; 2001US-0313377P.
                                                                                                                                                                         Chenault RA,
Fanger GR,
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                                                                                             GAAACCGAGCATAGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATG 100
                                                                630 GAAACCGAGCATAGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATG 689
                                                                                                                                                        221 GAACCTCTAGAAATGAAGGGATAGAAATCACAGAAGTAACTGCTTCCCCTGAGGATAAT 280
                                                                                                                                                                                                                                                                                                                                              GAAGAGATGATGTCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGAAGATGAA 749
                                                                                                                                                                                               750 AGATTGCACCATGATACAGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATAT 809
                                                                                                                                                                                                                   GAACCTCTAGAAAATGAAGGGATAGAAATCACAGAAGTAACTGCTCCCCCTGAGGATAAT 869
                                                                                                                                                                                                                                                                                                                              CCTGTAGAAGATTCACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAGAACAG 929
                                      Gaps
                                    ;
Query Match 10.7%; Score 249; DB 11; Length 495; Best Local Similarity 99.7%; Pred. No. 4.9e-105; Matches 299; Conservative 0; Mismatches 1; Indels (
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RESULT 20 ACH93769/c ID ACH93769 standard; DNA; 161 BP.

(first entry) 29-JUL-2004

Human genome derived single exon probe #26964.

Human; probe; ss; gene expression; single exon probe; microarray;. alternative splicing event; genomic alteration.

Homo sapiens.

US2003194704-A1.

16-OCT-2003.

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03-APR-2002; 2002US-00029386

03-APR-2002; 2002US-00029386

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

Penn SG, Rank DR, Hanzel DK;

WPI; 2004-119264/12.

New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.

Claim 1; SEQ ID NO 26964; 80pp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide compression, comprising any of the 27,400 fully defined nucleotide according a least 8 amino acids of any of the 6888 amino acid sequences for conditions at least 8 amino acids of any of the 6888 amino acid sequences for included are a spatially—

CC encoding at least 8 amino acids of any of the 6888 amino acid sequences (hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially—

CC expressed in human cells or tissues. Also included are a spatially—

CC and addressable set of single exon nucleic acid molecule or measuring human gene expression, a method of probes cited above, where each of the plurality of probes cited above, where each of the plurality of probes is separately

CC and addressably isolatable or amplifiable from the plurality, a single exon microarray for measuring human gene expression, a wethor of measuring human gene expression, a vector comprising at least 8

CC probe cited above, an ORF-encoded peptide comprising at least 8

CC contiguous amino acids of any of the above—mentioned amino acid sequences (Optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to thorage expression and acid a single exon probe crited above. The probes may be used as tools for surveying croage medium which contains a database having a plurality of records croage medium which contains a database having a plurality of records croage medium which contains a database having a plurality of records croage medium which contains a database having a plurality of records croage medium which contains a database having a plurality of records croage medium which contains a database having a tools croage medium which croage medium and contains and contains and contains and c segdata.uspto.gov/sequence.html?DocID=20030194704

Sequence 161 BP; 45 A; 49 C; 25 G; 42 T; 0 U; 0 Other;

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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expression human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human cells or amplifiable from the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of exon microarray for measuring human gene expression, a vector comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid so isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to methods of selling and/or licensing single exon probes or microarrays to methods of selling and/or licensing single exon probes or microarrays con thuman gene expression data by subscription, and a computer-readable catorage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                            110 GGAACTICETICACGIGGITTAIGGIGATIGCATIGCIGGGCGICIGGACAICTIGT 51
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, probe, ss, gene expression, single exon probe, microarray, alternative splicing event, genomic alteration.
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4.5%; Score 104; DB 12; Length 161;
                                                                                                                                                        222 GCTGTCGTTTGGTTTGATCTTGACTATGAGGAAGTTCTAGG 265
                                        Indels
                                                                                                                                                                            GCTGTCGTTTGGTTTGATCTTGACTATGAGGAAGTTCTAGG 7
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                    . 1.4e-37;
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              100.0%; Preα. ν...
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                                                                                                                                                                                                                                                                              069/c
ACH80069 standard; DNA; 592
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                          104; Conservative
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                    ACH80069;
      Query Match
Best Local
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cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alternative splicing events, in detecting and characterising gross smaller genomic alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=20030194704
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; gene therapy; protein therapy; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; autoimmune disease; AIDS; developmental abnormality; foetal deficiency; Alzheimer's disease; cognitive disorder; schizophrenia; immunological disorder; mood disorder; immune deficiency disease; respiratory disorder; arthritis; skeletal; hematopoiatic disorder; neural; osteoporosis; metabolic disorders;
                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, immune deficiency diseases or blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiovascular; endocrine; gastrointestinal; asthma; diagnosis;
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4.5%; Score 104; DB 12; Length 592;
Best Local Similarity 100.0%; Pred. No. 1.4e-37;
Matches 104; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                         Sequence 592 BP; 220 A; 122 C; 79 G; 171 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGTCGTTTGGTTTGATCTTGTTGACTATGAGGAAGTTCTAGG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAY01148, AAY01190, AAY01191, AAY01192, AAY01193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 GCTGTCGTTTGGTTTGATCTTGTCGACTATGAGGAAGTTCTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein gene 14 clone HAGBZ81.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 131; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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97US-0051480P.
97US-0058598P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX22124 standard; DNA; 1382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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12-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX22124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170
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The invention relates to nucleic acid sequences (AAX22111 to AAX22134) encoding human secreted proteins (AAX01155 to AAX01158). The secreted proteins (AAX01155 to AAX01158). The secreted protein gene sequences are deposited with the ATCC under deposit number and card sequences are deposited with the ATCC under deposit number nucleic acid sequences are used for the recombinant production of the nucleic acid sequences are used for the recombinant production of the nucleic acid sequences are used for the recombinant production of the nucleic acid sequences are useful for preventing, treating or ameliorating medical for are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Pathological conditions can be also dispnosed by determining the amount of the new polypebtides in a sample or by determining the presence of mutations in the new polypeptides in a polymucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foctal deficiencies, autoimmune diseases, lymphomas, Alzheimer's and cognitive disorders, autoimmune diseases, respiratory disorders, immune deficiency disorders, immune deficiency disorders, immune deficiency disorders, immune disorders, neural disorders, neural disorders, excleteral disorders, endocrine for identifying that binding partners. The present sequence represents a number and clone identification)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 AGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; cancer; hyperproliferative disorder; rheumatoid arthritis; autoimmune disorder; haematopoietic disorder; anaemia; allergic reaction; asthma; cardiovascular disorder; wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antialergic; hepatotropic; antidiabetic; antinflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match 3.1%; Score 72; DB 2; Length 138.
Local Similarity 100.0%; Pred. No. 1e-22;
les 72; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vulnerary; cardiant; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA39640 standard; cDNA; 1382 BP.
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM;
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Matches
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The invention relates to novel genes ADA39629-ADA40565 and proteins
ADA40566-ADA41501 for human secreted proteins, useful for preventing,
treating or amaliorating medical conditions e.g. by protein or gene
therapy. The polypeptides, nucleic acid molecules, antibodies or their
cuseful for preparing a diagnostic or pharmaceutical composition for
tragments, and agonists or antagonists that bind to the polypeptide are
useful for preparing a diagnostic or pharmaceutical composition for
cuseful for preparing a diagnostic or cher hyperproliferative disorder. The
polypeptides and nucleic acid molecules are also useful for detecting,
concern diagnosing, prognosticating, treating or ameliorating cancer
or other hyperproliferative disorders including neoplasms, autoimmune
disorders (e.g. diabetes, rheumatoid architis, systemic lupus
concern diabetes, rheumatoid architis, systemic lupus
anemia, haematopoletic or haematological disorders (e.g. anaemia,
thrombocytopenia), allergic reactions including asthms or eczema,
thrombocytopenia, allergic reactions including asthms or experimental
contained or viral infections including HIV/AIDS), or wound healing and
disorders of peithhelial cell proliferation. The nucleic acides are also
useful for chromosome identification, rediation hybrid and propertication
contained in chromosome identification, rediation hybrid and propertication
of the tissues immunohistopical probes for differential identification
of the tissues immunohistopical probes for differential identification
of the tissues immunohistopical probes of the parent did not form part of the printed specification, the patent did not form part of the printed specification or disappance.

This patent did not form part of the printed specification and print/published pot s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cardiant, antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                New human secreted proteins and nucleic acid molecules, useful for preparing a diagnostic or pharmaceutical composition for diagnosing preventing or treating cancer or other hyperproliferative disorder.
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100.0%; Pred. No. 1e-22;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                     Claim 9; SEQ ID NO 22; 3205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACC50349 standard; cDNA; 1382 BP.
                                                                                                                        asthma, allergies or AIDS.
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Best Local Similarity 100..
Best Anna 72; Conservative
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WPI; 2003-175238/17.
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WO200295010-A2.

28-NOV-2002.

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multiple sclerosis; ischaemic brain injury; Parkinson's disease;
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                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel human secreted proteins (ABR47633-6 ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arteriosclerosis and myocardial ischaemia), neural disorders, immune cystem disorders muscular disorders, pulmonary disorders, reproductive disorders; immune proliferative disorders and/or cancerous diseases and conditions, for treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or intection, for the analysis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or controlled or controlled or prevent skin aging or hair loss, to current and aid in tissue transplants or bone and periodontal regeneration and aid in tissue caramalist growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, to marrow cells when used in combination or the marrow cells when vesed eliferentiation or for supporting cell culture of primary crissues to increase or decrease differentiation or pranafation of primary contains and periodor and and profifered the marrow cells when the combination or for supporting cell culture of primary contains the marrow cells when the marrow cells when the cells when the cells when the cells when the marrow cells when the cells when th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 AGGAAAACTAGGAATCTATGATGCTGATGGTGATGAGATTTTGATGTGGATGATGCCAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 AGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAA 292
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                                                                                                                                                                                                                                       Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in electronic format and is available from WIPO at
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100.0%; Pred. No. 1e-22;
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ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                     Claim 21; SEQ ID NO 16; 1881pp; English
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                                                                                                                                                                                                                                                                               disorders such as arrhythmia.
                                               21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
           19-MAR-2002; 2002WO-US009785
                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
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es 72; Conservative
                                                                                                                                                                                                                                                                 diagnosing, prognosti
                                                                                                                                                                 Ruben SM;
                                                                                                                                                                                                     WPI; 2003-129429/12
                                                                                                                                                                   Ковеп СА,
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The invention relates to 592 new human secreted polypeptides useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or polypeptides comprising an amino acid neurodegenerative disorders, or polypeptides comprising an amino acid acids encoding the polypeptides, corporated that binds to the polypeptide, are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune compositions for diagnosing, treating or preventing an e.g. immune compositions for diagnosing, treating or preventing an e.g. immune compositions for diagnosing, treating or preventing an e.g. inflammatory bowel disease, nephritis or Crohn's disease, respiratory disorders (e.g. asthma and allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative cardiovascular disorders (e.g. atherosclerosis or myocarditis), and cardiovascular disorders (e.g. atherosclerosis or myocarditis). The polymoleotides are useful for chromosome identification, chromosome mapping, for controlling gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, for identification chromosome corresponders. The polypeptides are useful for as molecular weight markers on sodium dodecyl sulface-polyacrylamide gel electrophorasis (SDS-PAGS) censul, polliferative and/or cancerous diseases, This sequence corresponds to a gene encoding one of the polypeptide of the invention. Note: The sequence data for this patent did form part of the printed specification, to blt was obtained in electronic format directly from WIPO at the print of the print of the printed of the printed by the printed of the printed of the printed by the printed of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 AGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAA
Alzheimer's disease, atherosclerosis, myocarditis, chromosome mapping
triple helix formation, antisense gene therapy, forensic biology, ds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1382 BP; 413 A; 216 C; 288 G; 464 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 1e-22; rative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 21; SEQ ID NO 24; 1754pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAR-2002; 2002WO-US008278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-167512/16.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                WO2002102994-A2
                                                                                                                                                                                                         Homo sapiens.
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293 AGTTTTATTAGG 304

RESULT 26 ABN38322

ABN38322 standard; DNA; 60 BP.

ABN38322;

(first entry) 15-JUL-2002

Human spliced transcript detection oligonucleotide SEQ ID NO:11070.

Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.

Homo sapiens.

WO200210449-A2.

07-FEB-2002.

20-JUL-2001; 2001WO-IB001903.

28-JUL-2000; 2000US-0221607P. 02-MAY-2001; 2001US-0287724P.

(COMP-) COMPUGEN INC.

Mintz E, Mintz L, Faigler S; Shoshan A, Wasserman A,

WPI; 2002-257383/30.

New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes

Example 1; SEQ ID NO 11070; 47pp; English.

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptom, where the (sub1 transcription comprises messenger RNAs transcribed from multiple
configuration units that populate a genome. The library comprises several dignomicleotides, ach capable of hybridising selectively to a set of messenger RNAs transcription unit of the genome, which encodes one or more messenger RNAs splice variants. The coligonucleotide libraries are useful for detecting mRNAs from a libraries are useful for detecting mRNAs from a libraries are useful for detecting mRNAs from a libraries and splice variants of human or animal contractively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal contraction of the sub-transcriptome under a particular confogical or pathological state, and so allowing the detection of tissue contraction or pathological state, and so allowing the detect of tissue under a specific pathological condition, to detect despective contraction of the splice disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from caref, humans and milee, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form to per directly from WIPO at ftp. wipo.int/pub/published_pot_sequences

Sequence 60 BP; 22 A; 8 C; 17 G; 13 T; 0 U; 0 Other;

Query Match Best Loca Matches

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672 GACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAATCCAGATTCCAGTGAA 731 1 GACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAATCCAGATTCCAGTGAA 0; Gaps 2.6%; Score 60; DB 6; Length 60; 100.0%; Pred. No. 4.2e-17; tive 0; Mismatches 0; Indels Local Similarity 100.0

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9

Human BEC/LEC-related gene sequence SeqID487. 564/c ADN95564 standard; DNA; 2208 (first entry) 01-JUL-2004 ADN95564; RESULT 27

growth, differentiation, blood endothelial cell; BEC; lymbhatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3; lymphatic growth agent; VEGF-C; VEGF-D; antianglogenic; cytostatic; vasotropic; antiinflammatory; gene therapy; endothelial cell disorder; inflammatory disease; cancer metastasis; lymphatic system; gene; ds; human.

Homo sapiens.

WO2003080640-A1.

02-OCT-2003.

07-MAR-2003; 2003WO-US006900.

07-MAR-2002; 2002US-0363019P.

(LUDW-) LUDWIG INST CANCER RES. (LICN) LICENTIA LTD.

Petrova T, Saharinen P, Saharinen J; Alitalo K, Makinen T,

2003-876899/81. P-PSDB; ADN95563 Example 1; SEQ ID NO 487; 176pp; English.

This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprises contacting endothelial cells (LEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating heredicary lymphoedeam comprises dentifying a human subject with lymphoedeam and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedeam in human subjects, and with the provise that the LEC protein comprision of lymphatic growth agent selected from VEGF-C or correlates with lymphoedeam in human subjects, and with the subject a composition comprisions of lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polymucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, vascitorior or antiantialmancory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells in treating heredicament for the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the differential not blood vessel endothelial cells growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedeam resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels such as the treatment of hereditary lymphoedeam resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels, such as the captes in the present sequence is that of a human LEC/BEC differentially expressed gene which is related to the method of the invention. Not expense index a given in table 14 of the specification.

Sequence 2208 BP; 621 A; 428 C; 484 G; 675 T; 0 U; 0 Other;

ö 2.5%; Score 59; DB 11; Length 2208; 100.0%; Pred. No. 1.1e-16; Live 0; Mismatches 0; Indels (Best Local Similarity 100.0 Matches 59; Conservative Query Match

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Gaps

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This invention relates to the novel association of protein sequences (and the genes which encode them) to the NF-kappaB pathway. The invention may be useful for the production of compounds with an antinifianmancory, cytostatic, hepatotropic, virucide, antiarteriosclerotic, antiarheumatic, antiarteriosclerotic, antiarteriosclerotic, immunosuppressive or immunomodulator, cerebroprotective, vasotropic, immunosuppressive or vulnerary activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder, an inflammatory disorder as related to aberran NF-kappaB regulation, cancer, aberrant apoptosis, related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, spendromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HILV-1, hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide; KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic; antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic; My antiarterioscleroit; immunomodulator; cerebroprotective; vasotropic; immunosuppressive; vulnerary; gene therapy; immune disorder; kw immunosuppressive; vulnerary; gene therapy; immune disorder; kw inflammatory disorder; hypohidrotic ectodermal dysplasia; whyper-Igw syndrome; hypohidrotic ectodermal dysplasia; kw hyper-Igw syndrome; hypohidrotic ectodermal dysplasia; kw hyper-Igw syndrome; host cell survival; evasion of immune response; kw viral infection; HIV-1; HTIV-1; hepatitis B; hepatitis C; EBV; influenza; kw viral infection; HIV-1; hillammatory bowel disease; colitis; asthma; heterosclerosis; cachexia; euthyroid sick syndrome; stroke; EAB; kw alterosclerosis; cachexia; euthyroid sick syndrome; stroke; EAB; kw aberrant acute phase response; hypercongenital condition; birth defect; when the condition; wound; organ transplant rejection; when the cache is the cache in the cache is the cache is the cache is the cache is the cache in the cache is the cache is the cache is the cache is t
2239 GGCATCCGGAACTGACACACACAGCAGAGACGCCGTTCCAGCAATTTAGCATGAATTC 2297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
                                    59 GGCATCCGGAACTGACACCACAGCAGAGACGCAGCCTTCCAGCAATTTAGCATGAATTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                    Human NF-kappaB pathway-associated gene SeqID177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carman J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 177; 237pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nadler SG, Neubauer MG, Feder JN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV propagation; gene; ds; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                        ADR14176/c
ID ADR14176 standard; DNA; 2208 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-2003; 2003US-0440068P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAY-2003; 2003US-0469757P
                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                              21-OCT-2004
                                                                                                                                                                                                                                                                                                  ADR14176;
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The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antichemmatic, immunosuppressive, osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, antiasthmatic, hepatocropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
             bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper immune activity, disorders related to aberrant acute phase responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, organ transplant rejection, birth defects, necrotic lesions, wounds, organ transplant rejection, conditions related to organ transplant rejection, conditions is related to organ transplant proliferating disorders related to aberrant signal transduction, necessity with other viruses. The present sequence is that of a human gene which is subject to the novel association with the NF kappaB pathway of the invention. Note: This sequence does not appear in the specification but was obtained by the indexer from Genbank.
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                                                                                                                                                                                                                                                                                                                                                                                              2239 GGCATCCGGAACTGACACCACAGCAGAGACGCAGCCTTCCAGCAATTTAGCATGAATTC 2297
survival, evasion of immune responses, rheumatoid arthritis, inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                               GCCATCCGGAACTGACACACAGAGAGGAGCCTTCCAGCAATTTAGCATGAATTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                              DB 13; Length 2208; 1.1e-16;
                                                                                                                                                                                                                                                                       Sequence 2208 BP; 621 A; 428 C; 484 G; 675 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO polypeptide encoding cDNA SEQ ID NO:247.
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2.5%; Score 59; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 59; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                  2.5%; Score 59;
.00.0%; Pred. No.
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ID ADP23153 standard; cDNA; 2208 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-NOV-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-419628/39.
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juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an didopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune trombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Gulllain-Barre syndrome, chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infections or autoimmune chronic active hepatitis, primary inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, pneumonitis, a transplantation associated disease, graft rejection or graft ververs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2239 GGCATCCGGAACTGACACCACAGCAGAGACGCAGCTTCCAGCAATTTAGCATGAATTC 2297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 GGCATCCGGAACTGACACACACAGCAGAGACGCAGCTTCCAGCAATTTAGCATGAATTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; colon cancer; cancer; tissue profiling; forensic; mapping;
genetic analysis; diagnostic; antisense therapy; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human colon cancer related nucleotide sequence SEQ ID NO:3266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 2.5%; Score 59; DB 13; Length 2208; Local Similarity 100.0%; Pred. No. 1.1e-16; es 59; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2208 BP; 621 A; 428 C; 484 G; 675 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Catino TJ, Dwivedi P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carroll E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1; 796pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABQ59571 standard; cDNA; 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2001; 2001WO-US030732.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burgess C, Astle JH, Ca
Thiaglingam A, Lewis ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-426115/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200229086-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABQ59571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 30
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from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profilling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying an agent that modulates the function of an apoptosis-
associated polypeptide, useful for diagnosing or treating e.g. cancer,
comprises comparing the binding of the polypeptide to the candidate agent
and to a control agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to novel agents that modulates the function of buman apoptosis associated proteins specified within the specification. Specifically, it refers to a method for the identification of target genes whose expression is correlated with an early stage in the regulation of apoptosis. The present invention describes a method of contacting either candidate agents or control agents to the target genes and assessing the difference of binding and inhibitory activity, where the candidate agent is selected from a low molecular weight organic molecule, an antibody or fragment thereof, an antisense oligonucleotide, a small inhibitory disRNA, or a ribozyme. As such, the compositions and methods are useful for diagnosing and treating diseases or conditions associated with abnormal apoptosis in mammalian tissue, such as cancer, inflammation, autoimmune or neurodegenerative disorders. Accordingly, they exhibit cytostatic, antiinflammatory, immunosuppressive and
                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                             2274 CITCCAGCAATITAGCATGAATICATGCAAGCTTGGGAAACTCTGGAGAGA 2324
                                                                                                                                                                                                                                                                                                                                                                       88; apoptosis; cancer; inflammation; autoimmune; metrodegenerative disorder; cytostatic; antiinflammatory; immunosuppressive; neuroppretective; gene therapy; PCR; primer; real-time PCR; RT-PCR; CDIPT.
                                                                                                                                                                                                                                                        ch 2.2%; Score 51; DB 6; Length 583; l Similarity 100.0%; Pred. No. 6e-13; 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reverse quantitative PCR primer to amplify human CDIPT DNA.
                                                                                                                                                                                                               Sequence 583 BP; 170 A; 128 C; 126 G; 152 T; 0 U; 7 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keating KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Page 289; 304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EIRX-) BIRX THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAR-2004; 2004WO-GB000957.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR97461 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-662402/64.
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Best Local S
Matches 51
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Sequence 23 BP; 9 A; 5 C; 8 G; 1 T; 0 U; 0 Other;

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This invention relates to novel agents that modulates the function of human apoptosis-associated proteins specified within the specification. Specifically, it refers to a method for the identification of target genes whose expression is correlated with an early stage in the regulation of apoptosis. The present invention describes a method of contacting either candidate agents or control agents to the target genes contacting either candidate agents or control agents to the target genes and assessing the difference of binding and inhibitory activity, where the candidate agent is selected from a low molecular weight organic molecule, an antibacky or fragment thereof, an antisense oligonuclectide, as small inhibitory dSRNA, or a ribozyme. As such, the compositions and methods are useful for diagnosing and treating diseases or conditions associated with abnormal apoptosis in mammalian tissue, such as cancer, inflammation, autoinmune or neurodegenerative disorders. Accordingly, they exhibit cytostatic, antiinflammatory, immunosuppressive and control or neuroprotective activities. These may also be used for drug screening purposes and in gene therapy. This oligonucleotide sequence is a quantitative PCR primer used to amplify a target gene associated with an exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying an agent that modulates the function of an apoptosis-associated polypeptide, useful for diagnosing or treating e.g. cancer, comprises comparing the binding of the polypeptide to the candidate agent
neuroprotective activities. These may also be used for drug screening purposes and in gene therapy. This oligonucleotide sequence is a quantitative PCR primer used to amplify a target gene associated with apoptosis regulation, given in an exemplification of the invention.
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Forward quantitative PCR primer to amplify human Cathepsin Cl DNA.
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neurodegenerative disorder; cytostatic; antiinflammatory;
immunosuppressive; neuroprotective; gene therapy; PCR; primer;
real-time PCR; RT-PCR; Cathepsin C1.
                                                                                                                                                 Score 27; DB 13; Length 27;
Pred. No. 0.096;
                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seera L;
                                                                                                            Seguence 27 BP; 10 A; 11 C; 1 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayes I,
                                                                                                                                        1.2%; Sco...
100.0%; Pred. No. v...
0; Mismatches
                                                                                                                                                                                                                                     CTGATGGTGATGGAGATTTTGATGTGG 312
                                                                                                                                                                                                                                                                            CTGATGGTGAGATTTTTGATGTGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keating KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Page 289; 304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-2004; 2004WO-GB000957.
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                                                                                                                                                                                                                                                                                                                                                                                  ADR97432 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                           1 Similarity 100.
27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and to a control agent
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                                                                                                                                                                                                                                                                              27
                                                                                                                                                       Query Match
                                                                                                                                                                             Local
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                             RESULT 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                             Drosophila melanogaster genomic polynucleotide SEQ ID NO 29182.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 29182; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 855;
     Length 23;
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                               Indels
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      DB 13;
7;
1.0%; scc...
100.0%; Pred. No. ',
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers EW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22;
Pred. No.
                                                          106 CCCGGAGAGAGACAAAGCATGGA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCCGGAGAGAGACAAAGCATGGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 AGCAGCGGCAACAGCAGCAGCA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; PIC
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                                                                                                                                                     BP
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                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                      ABL25903 standard; DNA; 855
                                                                                                                                                                                                         (first entry)
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                   Local Similarity 100.
                                                                                                                                                                                                                                                                         pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                            VO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interactions.
                                                                                                                                                                                                         26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139
                                                                                                                                                                                ABL25903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes
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ABL19239
ID ABL19
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                                   Matches
                                                                                                                             RESULT 33
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and instructions in higher eukaryotes for the development of insectioides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG17) expressed DNA sequences (ABLIG176-ABLIG17), expressed DNA ABRIG170.). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic form part of the from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                              detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more sense from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 2227;
18;
                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 22853; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2227 BP; 565 A; 720 C; 628 G; 314 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.9%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 18; Matches 22; Conservative 0; Mismatches
                                                                                                                                              Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1201 CAGCGCAACAGCAGCAGCAGC 1222
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        23-MAR-2001; 2001WO-US009231.
                                            23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                          New isolated nucleic acid
genes from Drosophila and
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                                                                                                                                            Venter JC, Adams M,
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                                                                                                      (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                    interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and real-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                 Drosophila, developmental biology, cell signalling, insecticide, pharmaceutical, gene, ds.
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                                                                           Drosophila melanogaster genomic polynucleotide SEQ ID NO 9190.
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llarity 100.0%; Pred. No. 18;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 9190; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                           23-MAR-2001; 2001WO-US009231.
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                                     (first entry)
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                                     26-MAR-2002
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ABL19239;
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                                            capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell. interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins (ABBC101840-ABBL16175) and the encoded proteins (ABBC10173). ABBC2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila, developmental biology, cell signalling, insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genomic polynucleotide SEQ ID NO 21634.
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                                  The invention relates to an isolated nucleic acid detection
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                                                                                                                                                                                   Sequence 2855 BP; 711 A; 668 C; 706 G; 770 T; 0 U; 0 Other;
                                                                                                                                                                                                              0.9%; Score 22; DB 4; Length 2855;
100.0%; Pred. No. 18;
        Claim 1; SEQ ID NO 29179; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                          0; Indels
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity
Matches 22; Conserv
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                                              Gaps
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Length 3705,
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Pred. No. 18;
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DB .
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  0.9%; Score 22; DB
llarity 100.0%; Pred. No. 18;
Conservative 0; Mismatches
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
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Best Local Similarity
Matches 22; Conserv
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ABL09456
ID ABL09
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AC ABL09
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WO200171042-A2.

27-SEP-2001.

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insercitides. The invention this experise in the development of insercitides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABLi6175) and the encoded proteins (ABB57737-ABB7072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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/note= "oligo dT bases added to the 3' end to stabilise
binding"
                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 21631; 21pp + Sequence Listing; English.
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1 Similarity 100.0%; Pred. No. 17;
22; Conservative 0; Mismatches
                                                                                                                                                 Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1276 AGCAGCGGCAACAGCAGCAGCA 1297
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  23-MAR-2001; 2001WO-US009231.
                                      23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                               Venter JC, Adams M,
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                                                                                                    (PEKE ) PE CORP NY
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misc_feature
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and influencial interactions in higher eukaryotes for the development of insectioides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176, ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                                               Drosophila melanogaster expressed polynucleotide SEQ ID NO 22850.
                                                                                          developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 22850; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
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                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US009231,
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11-JUL-2000; 2000US-00614150.
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                                                                                        Drosophila; developmental
pharmaceutical; gene; ss.
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pharmaceutical; gene;
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P-PSDB; ABB65353.
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WPI; 2004-662402/64.
                                                                                                                       Canis familiaris.
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                                                                      Query Match
                                                                          Matches
                                                                                          RESULT 42
                                                                                             AAZ98400
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The invention provides a composition comprising at least one oligonucleotide, of 9-35 bases, that binds specifically to part of the oligonucleotide, of 9-35 bases, that binds specifically to part of the mRNA, expressed from the gene encoding a mammalian betal-adrenoceptor mRNA alters transcription of the mRNA in cells. The compositions are used to treat transcription of the mRNA in cells. The compositions are used to treat diseases associated with increased number or activity of the betal-adrenoceptor polypeptide, specifically hypertension and myocardial ischemia. The compositions can also be used to produce recombinant ischemia. The antisense oligos may also be used to offect the mRNA or related DNA, including visualization within a cell, to generate transgenic animals with altered betal-adrenoceptor activity, and to screen patients for susceptibility to hypertension of particular alleles of betal-adrenoceptor genes. The present sequence represents the polymuclectide sequence of the canine betal-adrenoceptor (GenBank Acon No: U73207)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated antisense oligonucleotide of 9-35 nucleotides in length, which specifically binds to a portion of an mRNA expressed from a gene encoding a mammalian betal-adrenoceptor (AR) polypeptide and alters the translation of the mRNA into the betal-AR polypeptide in a host cell expressing the mRNA. Also included are a
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100.0%; Pred. No. 2.,
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                          Example 4; Page 90-91; 144pp; English.
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nes 21; Conservative
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to novel agents that modulates the function of human apoptosis-associated proteins specified within the specification. Specifically, it refers to a method for the identification of target spens whose expression is correlated with an early stage in the regulation of apoptosis. The present invention describes a method of contacting atther candidate agents or control agents to the target genes and assessing the difference of binding and inhibitory activity, where the candidate agent is selected from a low molecular weight organic molecule, an antibody or fragment thereof, an antisense oligonucleotide, as small inhibitory dSRN, or a ribozyme. As such, the compositions and methods are useful for diagnosing and treating diseases or conditions associated with abnormal apoptosis in mammalian tissue, such as cancer, inflammation, autoimmune or neurodegenerative disorders. Accordingly, they exhibit cytostatic, antiinflammatory, immunosuppressive and purposes and in gene therapy. This oligonucleotide sequence is an siRNA oligo used to knockout expression of a human gene identified to be the contact on the contact of the contact on the regulation of a human gene identified to be
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                                                                                                                 Identifying an agent that modulates the function of an apoptosis-associated polypeptide, useful for diagnosing or treating e.g. cancer, comprises comparing the binding of the polypeptide to the candidate agent and to a control agent.
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                                                                                                                                                                                                                                                                                                                                          Example 5; Page 293; 304pp; English.
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recombinant vector comprising the antisense oligonuclectide, and a host cell comprising the vector. A composition comprising the antisense oligonuclectides is useful in the manufacture of a medicament for use in treating or ameliorating hypertension, hypertrophy and cardiac ischaemia in a mammal. A composition comprising the antisense oligonuclectides is also useful for reducing the level of betal-AR polypeptide, the transcription of betal-AR polypeptide specific mRNA in a mammalian host call, particularly human cell, and for decreasing blood pressure in a promoter capable of expressing the oligonuclectide in the cell. A promoter capable of expressing the oligonuclectide in the cell. A promoter capable of expressing the oligonuclectide in the cell. A composition comprising a selected nucleic acid segment that comprises polymuclectide in a full length betal-adrenoceptor antisense polymuclectide in a cell is also useful for reducing the level of betal-coligonuclectide in a cell is also useful for reducing the level of betal-coligonuclectide is also useful for other cardiovaccular diseases and cardiac dysfunction in humans. The present sequence is a mammalian betal-che a function in humans. The present sequence is a mammalian betal-che are a promoted to the cardiac dysfunction in humans. The present sequence is a mammalian betal-che are cardiac dysfunction in humans. The present sequence is a mammalian betal-che are cardiac dysfunction in humans. The present sequence is a mammalian betal-che are cardiac dysfunction in humans. The present sequence is a mammalian betal-che are cardiac dysfunction in humans. The present sequence is a mammalian betal-che are cardiac dysfunction in humans. The present sequence cardiac dysfunction in humans. The present sequence of the cardiac dysfunction in humans. The present sequence cardiac dysfunction in humans. The present sequence cardiac dysfunction in humans. The present sequence cardiac dysfunction in humans of the cardiac decreases and cardiac dysfunction in the cardiac dysfu
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X-linked proliferative disease; XLP, tuberculosis; AIDS; schistosomiasis; cancer; breast cancer; prostate cancer; leukemia; leprosy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New signaling lymphocyte activation molecule associated protein useful in the treatment of tuberculosis and AIDS.
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98US-0099160P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AR gene, ....
the invention
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The present sequence represents an antisense oligonucleotide which inhibits human aspartyl (asparaginyl) beta-hydroxylase (HAAH) gene.

Epidermal growth factor (EGF) -like domains of polypeptides are hydroxylated by HAAH enzymes. HAAH is used in the method of the invention. The specification describes a method for diagnosing a malignant neoplasm in a mammal. The method comprises contacting a body fluid with an antibody which binds to HAAH polypeptide under complex. The method is useful for diagnosing an analysman neoplasm in a bodily fluid e.g. central nervous system (CNS) derived body fluid, blood, serum, urine, saliva, sputum, lung effusion, and ascites fluid of mammal, where the neoplasm is derived from endodermal tissue and is selected from colon canner, breast cancer, pancreatic cancer, liver cancer of bile ducts, and cancer of the CNS. HAAH antibodies, linked to a cytotoxic agent, are useful for killing tumour cells
protein-mediated signal transduction in a patient. Upregulation of SAP family members can be used for the treatment of diseases involving insufficient antigen-specific T cell activation (e.g. X-linked proliferative disease (XLP), tuberculosis, AIDS, schistosomiasis) or cancer (e.g. breast cancer, prostate cancer, leukemia), or leprosy. Downregulation of SAP family members can be used for the treatment of diseases characterized by an excessive amount of antigen-specific T cell activation (e.g. autoimmune diseases). The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing malignant neoplasm in a mammal, involves contacting mammalian sample with antibody that binds to human aspartyl beta-hydroxylase polypeptide to form antigen-antibody complex and detecting the complex.
                                                                                                                                                                                                                                                                                 Gaps
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human asparyt) beta-hydroxylase; HAAH; malignant neoplasm; tumour;
antisense oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human aspartyl (asparaginyl) beta-hydroxylase antisense molecule.
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                                                                                                                                                                                                Sequence 4011 BP; 1125 A; 828 C; 885 G; 1173 T; 0 U; 0 Other;
                                                                                                                                                                                                                                      Score 21; DB 2; Length 4011;
Pred. No. 51;
                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                37 GCAGCGGCAACAGCAGCA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Page 57; 76pp; English.
                                                                                                                                                                                                                                                        l Similarity 100.0%; P. 21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF89814 standard; DNA; 20 BP.
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                                                                                                                                                                                                                                         0.98;
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Best Local S:
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF89814;
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AAF89814/c
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(first entry)

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Diagnosing malignant neoplasm in a mammal, involves contacting mammalia:
sample with antibody that binds to human aspartyl beta-hydroxylase
polypeptide to form antigen-antibody complex and detecting the complex.
                                                                                                                                                                                           Epidermal growth factor-like domain; EGF-like domain; cancer; human aspartyl beta-hydroxylase; HAAH; malignant neoplasm; tumour; antisense oligonucleotide; ss.
                                                                                                                                                                    Human aspartyl (asparaginyl) beta-hydroxylase antisense molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RHOD-) RHODE ISLAND HOSPITAL LIFESPAN PARTNER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wands JR, De La Monte SM, Ince N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Page 57; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-2000; 2000WO-US030738.
                                                      AAF89812 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-329171/34.
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                  RESULT 47
AAF89812/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing malignant neoplasm in a mammal, involves contacting mammalian sample with antibody that binds to human aspartyl beta-hydroxylase polypeptide to form antigen-antibody complex and detecting the complex.
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                                                                                                                                                                                                                                                                                                                                                                                Human aspartyl (asparaginyl) beta-hydroxylase antisense molecule.
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                                       Length 20;
                                                                               0; Indels
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Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 U; 0 Other;
                                       0.9%; Score 20; DB 4; Le
100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carlson RI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ince N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Page 57; 76pp; English.
                                                                                                                          1 CGGACCGTGCAATGGCCCAG 20
                                                                                                                                                 20 CGGACCGTGCAATGGCCCAG 1
                                                                                                                                                                                                                                                                 AAF89813 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-00436184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-2000; 2000WO-US030738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De La Monte SM,
                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-329171/34.
                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-1999;
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                                                                                     20;
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                                                                                                                                                                                                                                                                                                           AAF89813;
                                             Query Match
                                                                                     Matches
                                                                                                                                                                                                                              RESULT 46
AAF89813/
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contacting mammalian

Carlson RI;

99US-00436184.

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The present sequence represents an antisense oligonucleotide which inhibits human aspartyl (asparaginyl) beta-hydroxylase (HAAH) gene. Bepidermal growth factor (BGF)-like domains of polypeptides are hydroxylated by HAAH enzymes. HAAH is used in the method of the invention. The specification describes a method for diagnosing a malignant neoplasm in a mammal. The method comprises contracting a body fluid with an antibody which binds to HAAH polypeptide under complex forming conditions, and detecting the antigen—antibody complex. The method is useful for diagnosing and prognosing a malignant neoplasm in a health of complex in the condity fluid e.g. central nervous system (CNS)-derived body fluid, blood, serum, urine, saliva, subtum, lung effusion, and ascites fluid of mammal, where the neoplasm is derived from endodermal tissue and is selected from
                                                                                                                                                                                                                                                                                                                                                                             colon cancer, breast cancer, pancreatic cancer, liver cancer, cancer of bile ducts, and cancer of the CNS. HAAH antibodies, linked to a cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                            agent, are useful for killing tumour cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.0%; Pr
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ID ABS57871 standard; DNA; 20 BP.
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CGTGCAATGGCCCAGCGTAA 25

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CGTGCAATGGCCCAGCGTAA 1

15-AUG-2002. \$\$CCCCCCCCCCCCCCCCCCCCCCCCCCCCX

Human, 88, aspartyl (asparaginyl) beta-hydoxylase; HAAH; antisense; cytostatic; immunostimulant; antibody; neoplasm; tumour; FBSO; 86A; 5C7; 19B; brain tumour; apiloma; glioplastoma; astrocytoma; haemangioma; pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer; liver cancer; c metastatic CNS neoplasm

Homo sapiens.

US2002110559-A1.

17-MAY-2001; 2001US-00859604.

99US-00436184. 08-NOV-1999;

(WAND/) WANDS J R. (DMON/) DE LA MONTE S M.

(DEUT/) DEUTCH A H. (GHAN/) GHANBARI H A.

Deutch AH, Ghanbari HA; Wands JR, De La Monte SM,

WPI; 2003-066676/06.

Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue of mammal with detectably-labeled antibody which binds to human aspartyl (asparaginyl) beta-hydroxylase.

Example 6; Page 18; 34pp; English.

The invention relates to diagnosing a neoplasm and inhibiting tumour CC growth in a mammal, using an antibody that binds to human aspartyl captrownly beta beta bydroxylase (HAAH). Diagnosing a neoplasm comprises contacting a tissue with a detectably-labelled antibody where an increase in level of antibody binding at tissue site compared to the level of binding to normal non-neoplastic tissue indicates the presence of a comparation in non-neoplastic tissue site. Inhibiting tumour growth in mammal involves administering the antibody conjugated to a cytotoxic agent to a mammal. Also included are a method of conferring an immune response to a tumour call in a mammal, by administering the antibody, a method of inducing an HAAH-specific immune response in a mammal, by administering to the mammal can HAAH polypeptide (or a polymucleotide composition of HAAH comprising an extracellular domain and lacking a cytoplasmic domain of HAAH, and extracellular domain and lacking a cytoplasmic domain of HAAH, and extracellular domain and lacking a cytoplasmic domain of HAAH, when the comparison of antibody or its fragment which binds to HAAH (where the antibody is FB50, CC activity or alpha-ketoglutarate binding domain and appidermal growth factor (ESP)-like domain. The methods are useful for diagnosing neoplasm or response to a brain tumour cell (e.g. glioma, glioblastoma, astrocytoma or mammal, inhibiting tumour growth in a mammal, inhibiting tumour cell and for inducing a HAAH-specific immune response to a brain tumour cell and for inducing a HAAH-specific immune response to a prain tumour cell and for inducing a mammal, presponse to a conferring mannal, for conferring immune response to a cancer, pancreatic cancer, liver cancer and cancer, breast cancer, pancreatic cancer, liver cancer and cancer of the bile ducts of the bile or bright and method is also useful for diagnosing neoplasms of central nerv (CNS) e.g. primary malignant CNS neoplasms of both neuronal and gli cell origin and metastatic CNS neoplasms, and for disgnosing brain tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma. The present sequence represents a Human HAAH antisense oligonucleotide

Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 U; 0 Other;

Gaps ö 0.9%; Score 20; DB 8; Length 20; 100.0%; Pred. No. 1.7e+02; 0; Indels Similarity 100.0%; Pred. No. 1.7 20; Conservative 0; Mismatches Local Best Loca Matches

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20 CGGACCGTGCAATGGCCCAG 1

ABS57870

1870/c ABS57870 standard; DNA; 20 BP.

ABS57870;

(first entry) 06-FEB-2003 Human HAAH antisense oligonucleotide #2.

Human; 98; aspartyl (asparaginyl) beta-hydoxylase; HAAH; antisense; cytostatic; imminostatidhan; antibody; neoplasm; tumour; FB50; 964; 5C7; 198; brain tumour; glioma; glioblastoma; astrocytoma; haemangioma; pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer; liver cancer; cancer of the bile ducte; primary malignant CNS neoplasm; mecastatic CNS neoplasm;

Homo sapiens.

JS2002110559-A1.

15-AUG-2002.

17-MAY-2001; 2001US-00859604.

99US-00436184. 08-NOV-1999;

WANDS J R. DE LA MONTE S M. (WAND/) (DMON/)

(DEUT/) DEUTCH A H. (GHAN/) GHANBARI H A.

Deutch AH, Ghanbari HA; De La Monte SM, wands JR,

WPI; 2003-066676/06.

Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue of mammal with detectably-labeled antibody which binds to human aspartyl (asparaginyl) beta-hydroxylase.

Example 6; Page 18; 34pp; English.

The invention relates to diagnosing a neoplasm and inhibiting tumour of growth in a mammal, using an antibody that binds to human aspartyl (asparaginyl) beca-hydroxylase (HAAH). Diagnosing a neoplasm comprises contacting a tissue with a detectably-labelled antibody where an increase in level of antibody binding at tissue indicates the presence of a binding to normal non-neoplasmic tissue indicates the presence of a contacting the antibody conjugated to a cytotoxic agent to a mammal. Contacting the antibody conjugated to a cytotoxic agent to a mammal. Also included are a method of conferring an immune response to a tumour coll in a mammal, by administering the antibody, a method of inducing an HAAH polypeptide, or its degenerate variant), a fragment of HAAH comprising an antibody or its fragment and lacking a cytoplasmic domain of HAAH, an autibody or its fragment which binds to HAAH (where the antibody is FB50, controlly or 198), a hybridoma cell line chosen from hybridoma FB50, that so in a mammal, and affecting a cytoplasmic of main of HAAH, and a mammal, and affecting a cytoplasmic of main of HAAH, and a mammal, and affecting a cytoplasmic of main of HAAH, and a mammal, and affecting a cytoplasmic of main and apidermal growth carrier (EGF)-like domain. The methods are useful for diagnosing neoplasm correction a mammal, for conferring immune response to a pancratic carcinoma cell de. 3. glioma, glioblastoma, astrocytoma creponse in a mammal, for conferring immune response to a pancratic carcinoma cell and for inducing a HAAH-specific immune response to a cancer, pancratic cancer, liver cancer and cancer of the bile ducts. The method is useful for diagnosing malignant concer, pancratic cancer, liver cancer and cancer of the bile ducts. The method is useful for diagnosing neoplasms of central nervous system (CNS) e.g. primary malignant CNS neoplasms of central nervous system concer, pancratic cancer, liver cancer and cancer of the bile ducts.

1 CGGACCGTGCAATGGCCCAG 20

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The invention relates to diagnosing a neoplasm and inhibiting tumour growth in a mammal, using an antibody that binds to human aspartyl growth in a mammal, using an antibody that binds to human aspartyl captacognized (asparaginyl) beta-hydroxylase (HAAH). Diagnosing a neoplasm comprises contacting a tissue with a detectably-labelled antibody where an increase in level of antibody binding at tissue site compared to the level of binding to normal non-neoplastic tissue indicates the presence of a administering the antibody conjugated to a cytotoxic agent to a mammal. Also included are a method of conferring an immune response to a tumour cell in a mammal, by administering the antibody, a method of inducing an HAAH: specific immune response in a mammal, by administering to the mammal colypeptide, or its degenerate variant), a fragment of HAAH, an comprising an extracellular domain and lacking a cytoplasmic domain of HAAH, an comprising an cattacollular domain and lacking a cytoplasmic domain of HAAH, an comprising to the natibody or its fragment which binds to HAAH (where the antibody is FBSO, 86A, 5C7 or 198), a hybridoma cell line chosen from hybridoma FBSO,
                                                                                                                                                                                                                                                                        ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, 88; aspartyl (asparaginyl) beta-hydoxylase; HAAH; antisense; cytostatic; immunostimulant; antibody; neoplasm; tumour; FB50; 86A; 5C7; 19B; brain tumour; glioma; glioblastoma; astrocytoma; haemangioma; pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer; inver cancer; cancer of the bile ducts; primary malignant CNS neoplasm; metastatic CNS neoplasm;
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                                                                                                                                                                                                                                                                           Gaps
cell origin and metastatic CNS neoplasms, and for diagnosing brain tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma. The present sequence represents a Human HAAH antisense oligonucleotide
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                                                                                                                                                                                                    Score 20; DB 8; Length 20;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                       Seguence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                    Local Similarity 100.0%; Pred. No. 1.7 nes 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human HAAH antisense oligonucleotide #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Page 18; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                   6 CGTGCAATGGCCCAGCGTAA 25
                                                                                                                                                                                                                                                                                                                                                                                      CGTGCAATGGCCCAGCGTAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (asparaginyl) beta-hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  '869/c
ABS57869 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-2001; 2001US-00859604.
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                                                                                                                                                                                                                  0.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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DE LA MONTE S M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2002110559-A1.
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(DMON/) DE LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABS57869;
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activity or alpha-ketoglutarate binding domain and epidermal growth factor (EGF)-like domain. The methods are useful for diagnosing neoplasm factor (EGF)-like domain. The methods are useful for diagnosing neoplasm or seponse to a brain tumour growth in a mammal, conferting an immune response to a brain tumour conferring immune response to a mammal, for conferring immune response to a parcratic carcinoma cell and for inducing a HAAH-specific immune response in a mammal. The method is useful for diagnosing malignant cancer, pancreatic cancer, liver cancer and cancer of the bile ducts. The method is also useful for diagnosing neoplasms of central nervous system cancer, paintmary malignant CNS neoplasms of both neuronal and glial cell origin and metastatic CNS neoplasms, and for diagnosing brain tumours e.g. glioma, glioblastoma, astrocytoma or haemangloma. The present sequence represents a Human HAAH antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying an agent that modulates the function of an apoptosis-associated polypeptide, useful for diagnosing or treating e.g. cancer, comprises comparing the binding of the polypeptide to the candidate agent and to a control agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/note= "Oligo dT bases added to the 3' end to stabilise
binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to novel agents that modulates the function of human apoptosis-associated proteins specified within the specification.
HA386A, HA15CA and HA219B, and a fragment of HAAH which lacks enzymatic
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense PPIA siRNA oligomer to knockout apoptosis related gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ss; DNA/RNA hybrid; apoptosis; cancer; inflammation; autoimmune; neurodegenerative disorder; cytostatic; antiinflammatory; immunosuppressive; neuroprotective; gene therapy; siRNA; PPlA.
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1.7e+02;
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                                                                                                                                                                                                                                                                                        Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.0%; Pred. No. 1.7 tes 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                           0.9%; Score 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 293; 304pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                 11 AATGGCCCAGCGTAAGAATG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                   20 AATGGCCCAGCGTAAGAATG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR97507 standard; RNA; 21 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-662402/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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Specifically, it refers to a method for the identification of target genes whose expression is correlated with an early stage in the regulation of apoptosis. The present invention describes a method of contacting either candidate agents or control agents to the target genes and assessing the difference of binding and inhibitory activity, where the candidate agent is selected from a low molecular weight organic molecule, an antibody or fragment thereof, an antisense oligonucleotide, as mall inhibitory dispus, or a ribozyme. As such, the compositions and methods are useful for diagnosing and treating diseases or conditions and associated with abnormal apoptosis in mammalian tissue, such as cancer, inflammation, autoimmune or neurodegenerative disorders. Accordingly, neuroprotective activities. These may also be used for drug screening purposes and in gene therapy. This oligonucleotide sequence is an siRNA associated with the regulation of a human gene identified to be associated with the regulation of apoptosis, given in an exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
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80.0%; Pred. No. 1.7e+02;
Live 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                 Sequence 21 BP; 7 A; 3 C; 5 G; 2 T; 4 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1789 ACTGGAAGTTAATCCGAGAT 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ACUGGAAGUUAAUCCGAGAT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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                                                                                                                                                                                                                                                                                                                             of the invention.
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Matches
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cc expressed in human cells or tissues. Also included are a spatially-
caddressable set of single exon nucleic acid probes for measuring human

CC gene expression (comprising a plurality of single exon nucleic acid

probes cited above, where each of the plurality of probes is separately

and addressably isolatable or amplifiable from the plurality), a single

condition of the above method is single exon

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corrorage medium which contains a database having a plurality of records

correct in acidium malysis. The probes may be used as tools for surveying a specific exon, or in constructing genome-derived single exon microarrays.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant expression vector; transcription regulatory element;
Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seqdata.uspto.gov/sequence.html?DocID=20030194704
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100.0%; Pred. No. 1.6e+02
ive 0; Mismatches 0
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P-PSDB; ABO62587.
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ACH96138/c
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                     The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element, and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This sequence encodes a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stably transformed cells expressing endorphin, enkephalin and catecholamine - and artificial organs contg. them, useful for control of pain, esp. implanted in the CNS.
                                                                                                                   Gaps
                                                                                                                                                                                                                                                    Analgesic; pain; bioartificial organ; pro-opiomelanocotin; FOMC; beta-endorphin; CNTF; IgSP-hFOMC; 88.
                                                                                                                   ö
                                                                                                   Score 20; DB 11; Length 786;
Pred. No. 1.6e+02;
                                                                                   Sequence 786 BP; 129 A; 220 C; 235 G; 202 T; 0 U; 0 Other;
                                                                                                                  0; Indels
                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 1.6
Marches 20; Conservative 0; Mismatches
         Disclosure; SEQ ID NO 1933; 932pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      "hPOMC region"
                                                                                                                                                                                                                                                                                                                                                "IgSP region"
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                  294 chaccachachachachach 275
                                                                                                                                   38 CAGCGGCAACAGCAGCAGCA 57
                                                                                                                                                                                         AAT62523 standard; DNA; 849 BP
                                                                                                                                                                                                                                      IgsP-hPOMC fusion DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-00481917.
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/product=
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/*tag= e
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                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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A DNA sequence (AATG2523) comprising a fusion between 1g8P and human proposonelanocortin (POMC) DNA can be utilised in the construction of vectors for the expression of endorphin cpds. Cleavage enzymes present in host cells can generate a suite of endorphins from POMC, some or all of which have analgesic properties. A DNA sequence (see also AATG2524) in which the ACTH coding region of the POMC gene is deleted its preferred. Host cells transformed with vectors (or a single polycistromic vector) encoding analgesic opds. can be encapsulated to form bioartificial organs that are implanted into a patient for control of pain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianamentc; antiarthritic; cancer; antirheumatic; hepatotropic; cereborprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparastitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                     Sequence 849 BP; 176 A; 266 C; 286 G; 121 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                            Length 849;
                                                                                                                                                                                                                                                                                                                                                                         0.9%; Score 20; DB 2; Le:
100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Page 58; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 GCAACAGCAGCAGCGGC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA19178 standard; DNA; 900 BP
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2000US-0225266P.
2000US-0225267P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative
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Matches 20; Conserv
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14-AUG-2000;
14-AUG-2000;
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ABA19178/c
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Mon Mar 28 06:06:56 2005

Sequence 900 BP; 123 A; 288 C; 293 G; 196 T; 0 U; 0 Other;

2000US-0225268P.
2000US-022547P.
2000US-022547P.
2000US-0225758P.
2000US-022575P.
2000US-022681P.
2000US-022681P.
2000US-022924P.
2000US-022934P.
2000US-022934P. 2000US-023399P 2000US-0233400P 2000US-0233063P 2000US-0233063P 2000US-0234223P 2000US-0234223P 2000US-0234234P 2000US-0234234P 2000US-023493P 2000US-023493P 2000US-023493P 2000US-023493P 2000US-023493P 2000US-023498P 2000US-023498P 2000US-023498P 2000US-023498P 2000US-023698P 2000US-0237037P 2000US-0244617P 2000US-0246474P 2000US-0246475P 2000US-0246476P 2000US-0246476P 2000US-0246525P 2000US-0246526P 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 18-AUG-2000; 18-AUG-2000; 18-AUG-2000; 18-AUG-2000; 19-SEP-2000; 19-SE 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-CCT-2000; 20-CC

08-NOV-2000; 2000US-0246527P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246611P.
17-NOV-2000; 2000US-0246611P.
17-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024928F.
17-NOV-2000; 2000US-024928F.
17-NOV-2000; 2000US-024928F.
17-NOV-2000; 2000US-024928P.
17-NOV-2000; 2000US-024928P.
17-NOV-2000; 2000US-024928P.
17-NOV-2000; 2000US-02493P.
17-NOV-2000; 2000US-025116P.
0S-DEC-2000; 2000US-025118P.
0S-DEC-2000; 2000US-025118P.
0S-DEC-2000; 2000US-025118P.
0S-DEC-2000; 2000US-025118F.
0S-DEC-2000; 200US-025118F.
0S-DEC-2000; 200US-025118F.
0S-DEC-2000; 200US-025118F.
0S-DEC-2000; 200US-025118F.
0S-DEC-2000; 200US-025118F.
0S-D

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.

Disclosure; SEQ ID NO 11509; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are medical conditions e.g. by protein or gene therapy. The genes are closated from a range of human tissues disclosed in the specification. The nucleic caids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: a) cancer. e.g. breast and covarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune clisonical disease, altoimmune hawolytic anaemia, autoimmune thyvoiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular diseases e.g. cerebral anoxia and epilepsy; and (f) infections diseases such as wyocardial scheenias; (d) wound healing (e) infections diseases such as viral, bacterial, fungal and parasitic infections diseases such as viral, bacterial, fungal and parasitic the printed specification, but was obtained in electronic format directly way.

0.9%; Score 20; DB 5; Length 900;

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                                                                                                                                 Query Match
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               ö
                                                                                                                                                                                                                                     Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder; ss.
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               Gaps
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               Indels
    Pred. No. 1.6e+02;
                                                                                                                                                                                                                  Human PRO23 nucleotide sequence SEQ ID NO:64.
                Mismatches
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                                                                 764 GCAACAGCAGCAGCGGC 745
                                           62
                  ;
                                                                                                                                       AAC58389 standard; cDNA; 908 BP
                                           43 GCAACAGCAGCAGCGGC
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99US-0141037P.
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2000WO-US000219.
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      100.08;
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                                                                                                                                                                                            (first entry)
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Wood WI;
                   20; Conservative
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P-PSDB; AAB24079.
      Best Local Similarity
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                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, pro-opiomelanocortin; POMC; corticosteroid; pain; analgesic;
chronic inflammation; neuroendocrine; CRF; beta-endorphin; gene therapy;
corticotrophin-releasing factor; antiinflammatory; gene; ds.
astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AGC58242 to AAC5836 fepresent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC58367 to AAC58367 to AAB24089 represent human PRO polymorlectide and protein sequences given in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agent for reducing pain, useful particularly for chronic inflammatory pain, comprises a nucleic acid construct for local expression of
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                                                                                                                                                                                                                                                                                                Length 908;
                                                                                                                                                                                                                                    Sequence 908 BP; 173 A; 308 C; 310 G; 117 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wittig B, Stein C, Schaefer M, Schroff M, Junghans C;
Koenig Merediz SA;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human pro-opiomelanocortin coding sequence fragment.
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0.9%; Score 20; DB 6; Ler
0.9%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                          0.9%; Score 20; DB 3; Ler
100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 GCAACAGCAGCAGCAGCGGC 273
                                                                                                                                                                                                                                                                                                                                                                                                                 43 GCAACAGCAGCAGCGGC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL49917 standard; DNA; 936
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                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-682796/73.
                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                        present invention
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therappy. The human polynucleotide of the invention may have a use in gene therappy. The human cated to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorder, endocrine autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, developmental disorder, rediting informations caused by virus, bacteria, fungi or paramite. The diting molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence data for this patent is not represented to the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format catery from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                       Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Hartbharner TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banvilla SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RB, Spiro PA, Stewart RA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New diagnostic and therapeutic polymucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human modecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
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100.0%; Pred. No. 1.6
:ive 0; Mismatches
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                                                                                                          12-SEP-2003; 2003WO-US028227.
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ID ACN42013 standard; cDNA; 1039
                                                                                                                                              12-SEP-2002; 2002US-0410259P.
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nes 20; Conservative
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P-PSDB; ABM83362.
                                                                                                                                                                                                     (INCY-) INCYTE CORP.
                                    WO2004023973-A2
Homo sapiens.
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                                                                        25-MAR-2004
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dithp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                               Drosophila, developmental biology, cell signalling, insecticide, pharmaceutical, gene, ds.
                                                                                                                                                                           Drosophila melanogaster genomic polynucleotide SEQ ID NO 32866.
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0.9%; Score 20; DB 4; Le Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matchles 20; Conservative 0; Mismatchles 0;
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                                                               ABL27131 standard; DNA; 984 BP.
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11-JUL-2000; 2000US-00614150.
                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                    Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75.
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                                                                                                                                       26-MAR-2002
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                                                                                                   ABL27131;
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ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myers EW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li PWD,
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12-SEP-2002; 2002US-0410260P.
                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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Best Local Similarity 100.
Matches 20; Conservative
Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M,
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                                                                    WO200171042-A2.
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                                                                                                                                     27-SEP-2001
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ACN42012
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Marthshorne TA, Suchorolski MT, Altus GM, Pitte SJ, Blder LV;
Mooney EM, Delegeane AM, Branesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LLi,
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kitton SS;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Match 0.9%; Score 20; DB 13; Length 1039; Local Similarity 100.0%; Pred. No. 1.6e+02; tes 20; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 har
Stevens KA, bia..
Stevens KA, bia..
Peralta CH, Anderson ..
Pace RE, Spiro PA, Stewar
Trace RE, Spiro PA, Stewar
Trace RE, Spiro PA, Stewar
Trace RE, Spiro PA, Stewar
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ID ABL16775 standard; DNA; 1070 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page; 190pp; English.
                                                                                                                                                                                                                                                                                         2002US-0410259P.
2002US-0410260P.
                                                                                                                                                                                                                        12-SEP-2003; 2003WO-US028227
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                                                                                  WO2004023973-A2
                  Homo sapiens.
                                                                                                                                                                                                                                                                                            12-SEP-2002;
12-SEP-2002;
                                                                                                                                                       25-MAR-2004
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Matches

RESULT 61

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Gaps

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A color polynucleotide of the invention may have a use in gene therappy. The human diagnostic and therapeutic polynucleotides (dithp) or polypepides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine disorder, entoimmune/inflammatory disorder, developmental disorders, or infections caused by virus, becaria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germine polymorphisms, as molecular weight markers, and for somatic or germine therapy. The present sequence represents a dithp polymucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format the way also at waw.wipo.int/pct/en/sequences/listing.htm
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP, Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL, Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
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                                                                                                                                                                                           New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shen F;
5J, Elder LV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human diagnostic and therapeutic polynucleotide SEQ ID NO:886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 13; Length 1088;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1088 BP; 219 A; 358 C; 368 G; 143 T; 0 U; 0 Other;
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.9%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 1.6 Matches 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACN42011 standard; cDNA; 1089 BP.
                                                                                                    Suarez CJ;
                                                                                                                                                                                                                                                                                         Claim 1; Page; 190pp; English.
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                                                                                                                                    WPI; 2004-329368/30.
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                                                                            Kwong M, Po
S, Shi X,
                                                                                                                                                      P-PSDB; ABM83360
                                                                                                                                                                                                                                                        gene mapping.
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                                                                                               Patury S,
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A color polynucleotide of the invention may have a use in gene therappy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine continument/inflammatory disorder, developmental disorders, or autoimmune/inflammatory disorders, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp from minute biological samples, in detecting single nucleotide from molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide of polymorphisms, as molecular weight markers, and for somatic or germine gene therapy. The present sequence represents a dithp polynucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format weight markers with particular weight was obtained in electronic format the printed specification, but was obtained in electronic format was warmed to the present sequence data for this patent is not represented the manner of the printed specification, but was obtained in electronic format was a first parent sequence data for the present sequence data for this patent sequence data for this patent sequence format the printed specification, but was obtained in electronic format was sequenced and sequenced sequenced and sequenced sequenced and sequenced seq
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                                                                                                                                                                                                                                                                                New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
Delegeane AM, Panesar IS, Banville SC, Reddy TP, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; G M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen Shi X, Suarez CJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein gene 70 clone HCHMX01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            464 GCAACAGCAGCAGCAGCGGC 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 GCAACAGCAGCAGCGGC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ24880 standard; DNA; 1109 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page; 190pp; English.
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                                                                                                                                                                                              WPI; 2004-329368/30.
P-PSDB; ABM83359.
                                                                                                              Xu Y, Kwong M, Po
Patury S, Shi X,
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Mooney EM, D
Stevens KA,
Peralta CH,
Lagace RE, S
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ID AAZ2
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98US-0078563P.

19-MAR-1998;

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31-DEC-2001;
17-APR-2002;
15-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a nucleic acid molecule which encodes a secreted thuman protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion.

(e.g. AAZ24802) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 95 novel genes and their fragments (nucleic acid sequences: AAZ4811.224907, amino compared to the human protein only. The invention relates to 95 novel genes and their fragments (nucleic acid sequences: AAZ4811.224907, amino compared to medical conditions e.g. by protein or gene therapy. Also, or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypucleotides. Specific uses are described for each of the in the new polynucleotides. Specific uses are described for each of the in (see AAZ24811 for described uses)
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                                                                                                                                                                                                                                                                                                Yu G, Young PE, Feng P, Soppet DR;
, Kyaw H, Ebner R, Lafleur DW, Olsen HS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human genes, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 340-341; 484pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 gchacagcagcagcagcagc 133
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                                                                                    9805-0078577P
9805-0078578P
9805-0078579P
9805-0078581P
9805-0080312P
9805-0080312P
                                                                                                                                                                                                                                                                                                    Ni J, Rosen CA, Y
dress GA, Duan RD,
                        98US-0078573P.
98US-0078574P.
98US-0078576P.
                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                             Endress GA,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                      Ruben SM, Ni J,
Wei Y, Endress GA
Shi Y, Moore PA;
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                                                                   19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
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01-APR-1998;
                                                                                                                                                                                                                        01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders.
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                                                                                                                                                                                                                Novel isolated and purified nucleic acid molecule encoding beta-
endorphin, useful for treating a patient for psychological dependence on,
and abuse of, substances which have a stimulating and euphoric effect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOVX; antidiabetic; anorectic; cardiant; hypotensive; antidiabetic; anorectic; cardiant; hypotensive; antidiaterosclerotic; virucide; antiparkinsonian; anticonvilsant; osteopathic; antiarthritic; antiinflammatory; dermatological; antiathmatic; antilipaemic; metabolic; diabetes; obesity; infectious; anorexia; cancer; cardiovascular; hypertension; atherosclerosis; netrodegenerative; Alzheimer's disease; parkinson's; epilepsy; immune; osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia; neurogenesis; cell differentiation; proliferation; haemopoiesis; wound healing; anglogenesis; gene therapy; chromosome mapping;
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0.9%; Score 20; DB 3; Length 1230;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 3-4; 8pp; Norwegian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue typing; human; ss; gene; NOV
                                                                                                           Berg K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 GCAACAGCAGCAGCAGCGGC 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE28660 standard; cDNA; 1245 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 GCAACAGCAGCAGCGGC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NOV11a cDNA - SEQ ID 37.
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2001US-0341346P.
2001US-0341477P.
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2001US-0342592P.
2001US-0344297P.
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2002US-0373288P.
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98NO-00004992
                                                                                                              Alestrom P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2004 (first entry)
                                                                                                                                                                     WPI; 2000-373908/32
                                                       (GENO-) GENOVA AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003040330-A2.
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20-DEC-2001;
27-DEC-2001;
                                                                                                              Fagerlund TH,
27-OCT-1998;
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12-DEC-2001;
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us-09-436-184-3.oligo.rng

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Human, NOVX, gene; ss; congenital heart defect; cardiomyopathy; atherosels; Appertension; pulmonary stenosis; acleroderma; adenocarcinoma; haemophilia; graft-versus-host disease; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; multiple sclerosis; diabetes; obestiry; bronchial asthma; acquired immunodeficiency syndrome; AlDS; Crohn's disease; infectious disease; anorexia; immune disorder.
                                                                                                                                                                                                                                                                                                22-OCT-2001; 2001US-00035568.
05-NOV-2001; 2001US-033662F-
09-NOV-2001; 2001US-0345398P-
09-NOV-2001; 2001US-034833P-
15-NOV-2001; 2001US-033812F-
21-NOV-2001; 2001US-033152F-
28-NOV-2001; 2001US-03312F-
29-NOV-2001; 2001US-033132F-
29-NOV-2001; 2001US-033812F-
29-NOV-2001; 2001US-0343400F-
15-MAY-2002; 2002US-03869F-
16-MAY-2002; 2002US-0381048F-
02-JUL-2002; 2002US-0391348P-
02-JUL-2002; 2002US-0391348P-
02-JUL-2002; 2002US-0401479F-
06-AUG-2002; 2002US-0401626F-
07-AUG-2002; 2002US-0401626F-
07-AUG-2002; 2002US-0401659F-
07-AUG-2002; 2002US-0401659F-
                                                                                                                                                                                                                                                                  35-NOV-2002; 2002US-00287971
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ALVAREZ E.
ANDERSON D W.
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LEPLEY D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BARON M.
BOLDOG F L.
BOLDOG F L.
CHARAN S J.
CHAROVAL A.
DHANABAL M.
EDINGER S R.
ELISEN A.
ELLERMAN K.
ETTENBERG S.
GANGOLLI E A.
GERLACH V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MACDOUGALL J F
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCQUEENEY K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PADIGARU M.
PATTURAJAN N
PENA C E A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GORMAN L.
GROSSE W M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HACKETT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEZES P S.
MILLER C E
MILLET I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEKUDA R.
                                                                                                                                                                                          JS2004067882-A1.
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                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                38-APR-2004.
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(ALSO)
(ALVA)
(ALVA)
(BARC)
(BOLD)
(BOLD)
(CHAP)
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(HACK/)
(JIWW/)
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KHRA/)
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(MCQU/)
(MEZE/)
(MILL/)
(MISH/)
(PADI/)
(PATT/)
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        The invention relates to a novel isolated NOVX polypeptide. The polypeptide of the invention demonstrates, antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, virucide, antibacterial, fungicide, proteozoacide, nockropic, meuroprotective, antiparkinsonian, anticonvulsant, osceopathic, antiarthritic; antiparkinsonian, dermacological, antiasthmate and antilipaemic activities. The polypeptides, nucleic acid molecules and antilipaemic activities. The polypeptides, nucleic acid molecules and antilogement as section of diseases including metabolic disorders such as cradiovascular diseases including metabolic disorders such as cardiovascular diseases including metabolic disorders such as cardiovascular diseases including hypertension and atherosclerosis, cardiovascular diseases including hypertension and atherosclerosis, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease and epilepsy, immune disorders, asthma and dyslipidaemia.

The neurodegenerative disorders caids and polypeptides may also be used to identify molecules that modulate or inhibit neurogenesis, cell anglogenesis, as well as in gene therapy. Finally, the nucleic acids may be used as hybridiation probes, in chromosome mapping, tissue typing, be used as hybridiation probes, in chromosome mapping, tissue typing, the human NOV cDNA of the invention.
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                                                                                                                                                                                                 Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL; Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A; Elerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L; Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khrantsov NV; Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K; Mezes SS, Millet CE, Millet I, Mishra VS, Padigaru M, Patturajan M; Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA; Smithson G, Starling G, Spytek KA, Stone DJ, Tcherney VT, Twomlow N; Vernet CAM, Zerhusen BD, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated NOVX polypeptides and polynucleotides, useful for .. 
preventing, diagnosing or treating NOVX-associated disorders, e.g. 
osteoarthitis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.9%; Score 20; DB 10; L 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 37; 447pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 GCAACAGCAGCAGCAGCGGC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADM93405 standard; cDNA; 1245 BP
17-MAY-2002; 2002US-0381495P.
28-MAY-2002; 2002US-0383534P.
29-MAY-2002; 2002US-0383629P.
29-MAY-2002; 2002US-0384024P.
07-AUG-2002; 2002US-041788P.
26-AUG-2002; 2002US-0401788P.
31-OCT-2002; 2002US-0401533P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NOVX polynucleotide #19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Conservative
                                                                                                                                                                   (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-441555/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; ADE28661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM93405;
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ADM93405/
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XEXEXEX

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Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog rw, Alsobrook JP, Chapoval A, Dhanabal M, Edinger SP, Eisen A, Blargess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SP, Eisen A, Bilerman K, Ettenberg S, Gangolli EA, Gerlach V, Gorman L, Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV; Grosse WM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K, Mazes PS, Miller CE, Miller I, Mishra V, Padigaru M, Patturajan M, Pena CEA, Peyman JA, Rastelli L, Rieger DK, Rothenberg ME; Shenoy SG, Shimkets RA, Smithson G, Spaderna SK, Starling G; Shenoy SG, Shimkets VT, Twomlow N, Vernet CAM;
                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated NOVX polypeptide useful treating or preventing disorders or syndromes such as Alzheimer's disease, Parkinson's disease, multiple sclerosis, diabetes, obesity, cancer, bronchial asthma, Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1245 BP; 170 A; 486 C; 407 G; 182 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 37; 330pp; English.
PEYMAN J A.
RASTELLI I.
RIEGER D K.
ROTHENBERG M E.
SHENOY S G.
SHIMKETS R A.
SHIMKETS R A.
SALDERNA S K.
SPADERNA S K.
STARLING G.
SPADERNA S K.
STONE D J.
                                                                                                                                                          VERNET C A M.
ZERHUSEN B D.
VOSS E Z.
                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-355303/33.
                                                                                                                                             TWOMLOW N.
                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ADM93406.
                                                                                                                                                                                             ZHONG M.
                                                (SHEN/)
                                                                                                (STAR/)
(SPYT/)
(STON/)
(TCHE/)
(TWOM/)
                                                                                                                                                                                  (VOSS/)
                                                                                                                                                           (VERN/)
                                                                                    SPAD/)
                          RIEG/
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The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The NOVX polypeptides and polynucleotides are useful for encoding them. The NOVX polypeptides and polynucleotides are useful for etermining the presence of or predisposition to a disease associated with altered levels of the sequences in a mammalian subject, and for treating or preventing a pathology associated with NOVX. The polypeptides are useful for treating or preventing disorders or syndromes such as congenital heart defects, cardiomyopathy, atheroscierosis, hypertension, pulmonary stenosis, soleroders or sheroscierosis, hypertension, pulmonary stenosis, soleroderma, adenocarcinoma, haemophilia, graft-versus-host disease, cancer, neurodegenerative disorders, Alzheimer's disease, parkinson's disease, multiple sclerosis, diabetes, obesity, bronchial asthma, acquired immunodeficiency syndrome (AIDS), Crohn's disease, parkinson's disease, anorexia and immune disorders. This sequence represents a human NOVX polynucleotide of the invention. Note: The sequence data for this patent is also available from USPTO at sequence.uspressor.
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                              Gaps
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Length 1245;
                              0; Indels
Score 20; DB 12; I
Pred. No. 1.5e+02;
                Local Similarity 100.0%; Pred. No. 1.5
nes 20; Conservative 0; Mismatches
                                                                                          138 gczacaccaccaccaccac 119
                                                             62
                                                             GCAACAGCAGCAGCGGC
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0.9%;

Query Match

Matches

43

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Length 1418; 0.9%; Score 20; DB 10; I 100.0%; Pred. No. 1.5e+02; Best Local Similarity Query Match

BP.

ACC79031/c ID ACC79031 standard; cDNA; 1418 XX AC ACC79031; AC ACC79031; DT 30-JUL-2003 (first entry)

ARE ACC79026 to ACC79105 encode the human secreted proteins (1) given in ABE56726 to ABE56805, designated SECP-1 to SECP-80. SECP sequences can ABE56726 to ABE56805, designated SECP-1 to SECP-80. SECP sequences can care the secretary of the target polymorphics of the target polymorphics of the target polymorphics of the target polymorphics of the secretary of the polymeptide of the target polymorphic of the polymeptide of the target polymorphic the secretary of the polymeptide of the secretary of the polymeptide of the secretary of the polymeptide of the secretary of the secret anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; thyromimetic; gene therapy; cancer; cell proliferative disorder; atherosclerosis; neurological disorder; and epilepsy, Huntington's disease; stroke; immune disorder; allergy; AIDS; inflammatory disorder; developmental disorder; hypothyroidism; Cushing's syndrome; infection; gene; ss. New human secreted proteins (SECP), useful for diagnosing, treating preventing diseases or conditions associated with the aberrant SECP expression e.g. cancer, AIDS, atherosclerosis, Huntington's disease, stroke, infections. Lal PG, Yue H, Honchell C, Baughn MR, Duggan BM, Tran UK; Tue Hrw Lee S, Thangavelu K, Yue H Tang TY, Warren BA, Gietzen KJ, Lal PG, Yue H, Honchell CD; Lehr-Mason PM, Burford N, Xu Y, Baughn MR, Duggan BM, Tran UK, Lee BA, Forsythe IJ, Richardson TW, Lee S, Thangavelu K, Yue F Emerling BM, Walla NK, Azimzai Y, Sanjanwala B, Hafalia AJA; Borowsky ML, Nguyen DB, Ison CH, Astromoff A, Ding L, Lee SY; Becha SD, Ramkumar J, Gandhi AR, Jin P, Fu GK, Swarnakar A; secreted protein; SECP; cytostatic; antiarteriosclerotic; Sequence 1418 BP; 168 A; 542 C; 442 G; 266 T; 0 U; 0 Other; Human secreted protein SECP-6 encoding cDNA SEQ ID NO:86. Claim 5; Page 246; 286pp; English. 20010S-0317818P 20010S-0317824P 20010S-0324040P 20010S-032468P 20010S-0343980P 20010S-034229P 20020S-0357022P 20020S-0362439P 2001US-0313249P. 2001US-0314752P. 2002US-0376988P 15-AUG-2002; 2002WO-US027143 (INCY-) INCYTE GENOMICS INC. WPI; 2003-278569/27. P-PSDB; ABR56731 WO2003016506-A2 Homo sapiens. 17-AUG-2001; 24-AUG-2001; 07-SEP-2001; 07-SEP-2001; 21-SEP-2001; 24-SEP-2001; 02-NOV-2001; 28-NOV-2001; 13-FEB-2002; 06-MAR-2002; 19-MAR-2002; 30-APR-2002; 27-FEB-2003

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Plant; maize; rice; sorghum; thale cress; soybean; wheat; transgenic; osmocic stress; sugar transport; cell cycle pathway; plant height; carbohydrate transport; crop productivity; plant growth; stress resistance; disease resistance; insect resistance; heat tolerance; nincogan assimilation; water stress tolerance; photosynthetic carbon fixation; virus resistance; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide, useful for manipulating plant protein quality, improving plant growth, yield and crop productivity or grain composition or producing plants with improved properties.
                       Polynucleotide sequence #280 useful in producing transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 280; 144pp; English.
                                                                                                                                                                                                                                                                             04-DEC-2002; 2002US-00310154.
                                                                                                                                                                                                                                                                                                               04-DEC-2001; 2001US-0337358P.
                                                                                                                                                                                                                                                                                                                                                                                                                  Edgerton MD, Chomet PS,
                                                                                                                                                                                                                                                                                                                                            (EDGE/) EDGERTON M D. (CHOM/) CHOMET P S. (LACC/) LACCETTI L B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-061374/06.
P-PSDB; ADM48230.
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                                                                                                                                                                                                           UŠ2003233670-A1.
                                                                                                                                                                            Oryza sativa.
                                                                                                                                                                                                                                              18-DEC-2003.
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Matches
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ID ADA7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                         Drosophila melanogaster expressed polynucleotide SEQ ID NO 7061.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20; DB 4; Length 1565;
Pred. No. 1.5e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 7061; 21pp + Sequence Listing; English.
   Indels
   ö
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.0%; Pred. No. 1.5 tes 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers EW;
                                                                 138 GCAACAGCAGCAGCGGC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 GCACAGCAGCAGCAGCGGC 253
                                43 GCAACAGCAGCAGCAGCGC 62
                                                                                                                                                     ABL04193 standard; cDNA; 1565 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000; 2000US-0191637P, 11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADM47862 standard; DNA; 1891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 98:0
                                                                                                                                                                                                                      (first entry)
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20; Conservative
                                                                                                                                                                                                                                                                                                             pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-656860/75.
P-PSDB; ABB60090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                             WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interactions.
                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2001.
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                                                                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                       ABL04193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADM47862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
 Matches
                                                                                                                  RESULT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                       ABL04193
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Laccetti LB;

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The present invention relates to polynucleotide sequences, and the proteins they encode. The sequences are isolated from a variety of proteins they encode. The sequences are isolated from a variety of corganisms such as plants (e.g. maize, rice, sorghum, thale cress, organisms such as plants (e.g. maize, rice, sorghum, thale cress, the production and wheat), cyanobacteria, bacteria, yeast and other fungi. The polynucleotide and polypoptide sequences of the invention are useful in comparing fertile transgenic plants, preferably maize, with desired phenotypes. The polynucleotide and polypoptide sequences are useful for improving plants by providing protection against comporting the cell cycle pathway, reducing blant height, modifying complexity improving plant height, modifying the cell cycle pathway, reducing plant height, modifying carbohydrate transport, improving disease resistance, improving disease resistance, improving corp productivity, improving plant growth and stress resistance, improving disease resistance, improving cold or heat tolerance, improving nitrogen assimilation, improving stalk serength, improving blotic and abjoric increased vigour, reducing senescence, and conferring virus resistance. The present sequence data for this patent is not provided in the printed specification but is obtained in electronic format from the USPTO printled specification but is obtained in electronic format from the USPTO
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00.0%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1891 BP; 379 A; 669 C; 494 G; 349 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1125 GCGCCACCAGCAGCAGC 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 GCGCCAACAGCAGCAGC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA71941 standard; DNA; 2000 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    website at segdata.uspto.gov.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Conservative
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a 8

ADA71941

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The invention relates to plant nucleotide sequences that direct seed-, cor constitutive transcription of an operatively linked nucleic acid sequence. The invention also relates to a method for augmenting a plant segment. The invention also relates to a method for augmenting a plant segment. The invention also relates to a method for augmenting a plant companies of altered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, corsphum, rice or wheat. The polynucleotides and the polypeptides they encode are useful for manipulating crop plants to alter or improve phenotypic characteristics, to produce large quantities of oil or proteins, to incur resistance to insecticides, viruses or fungi, and to incur stress tolerance (e.g. salt, cold or drought) to ensure the plants incur stress tolerance (e.g. salt, cold or drought) to ensure the plants carly flowering or altered metabolic pathways. This sequence or expresents a plant nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2000 BP; 649 A; 375 C; 340 G; 630 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moughamer T, Briggs SP, Cooper B, Glaz
tagiri F, Kreps J, Provart N, Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. .v..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 44; SEQ ID NO 2021; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 TGCTGATGGTGATGGAGATT 303
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                                                                                                                                       26-SEP-2001; 2001US-0325277P.
26-SEP-2001; 2001US-0325448P.
04-APR-2002; 2002US-0370620P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 98;
                                                                                                26-SEP-2002; 2002US-00260238.
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Les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Katagiri F,
                                                                                                                                                                                                                                                                                                      GLAZEBROOK J.
GOFF S A.
KATAGIRI F.
                                                                                                                                                                                                                                          MOUGHAMER T.
BRIGGS S P.
COOPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-190374/18
                                                                                                                                                                                                                             BUDWORTH P.
                                                                                                                                                                                                                                                                                                                                                                    KREPS J.
PROVART N.
RICKE D.
ZHU T.
                     US2004016025-A1
                                                         22-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goff SA,
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                                                                                                                                                                                                                             (BUDW/)
                                                                                                                                                                                                                                                (MOUG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                  (ZHUT/)
                                                                                                                                                                                                                                                                                                                                                                                          (PROV/)
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                                                                                                                                                                                                                                                                                                                                                     (KATA/)
                                                                                                                                                                                                                                                                                                                                                                        KREP/)
                                                                                                                                                                                                                                                                                                                                                                                                               (RICK/)
                                                                                                                                                                                                                                                                                                            GLAZ/
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g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. MI comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant, gene; ss; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet; smalze; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; cold tolerance; drought tolerance; plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            t t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                          Plant; bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zon G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.9%; Score 20; DB 8; Length 2000;
100.0%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2000 BP; 649 A; 375 C; 340 G; 630 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Glazebrook J, Goff SA, Hou
Whitham S, Xie Z, Zhu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID NO 5266; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 TGCTGATGGTGATGGAGATT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                686 TGCTGATGGTGATGGAGATT 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Cooper B,
S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                       22-JUN-2001; 2001WO-IB001105.
                                                                                                                                                                                                                                                                                                              22-JUN-2001; 2001WO-IB001105
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                                               20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
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                                                                                   SEQ ID 5266
                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W, Co
F, Quan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-175290/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant cDNA #2021.
                                                                                                                                                                                                                                   WO2003000898-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacterial, fung
illustrate the
                                                                                                                                                                                          Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004
                                                                                                                                                                                                                                                                          03-JAN-2003.
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antifungal
                                                                                        Rice gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota
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Katagiri
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                                                                                                                                                      gene; ds.
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Matches

ð g ADJ41021

Glazebrook J;

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Gaps

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Indels

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Score 20; DB 12; Length 2000; Pred. No. 1.5e+02;

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

30-MAR-2001; 2001WO-US008631.

WO200175067-A2.

11-OCT-2001.

Homo sapiens

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

Tang YT;

Ormanac RT, Liu C, WPI; 2001-639362/73

P-PSDB; ABG07948.

(HYSE-) HYSEQ INC.

DNA encoding novel human diagnostic protein #7939.

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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligomucleotide complementary to the complementary strand of a polymucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the compination of an oligomucleotide comprising a sequence complementary to the complementary strand of a polymucleotide which comprises a 5'-end complementary strand of a polymucleotide which comprises a 5'-end sequence and an oligomucleotide comprising a sequence complementary to a polymucleotide comprises a 1'-end sequence complementary to a polymucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are as an eased in antisense therapy and in gene therapy. The primers are useful for synthesising polymucleotides, particularly full-length cDNAs. The primers are also useful for the primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length CDNAs asily without any specialised methods. AAH13634 to AAH13638 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                      Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Human cDNA sequence SEQ ID NO:18501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.AUG-1999; 99JP-00300253.
11.JAN-2000; 2000JP-00118776.
02.MAY-2000; 2000JP-00133767.
09.JUN-2000; 2000JP-002418997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-00248036.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUL-1999;
                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                             EP1074617-A2
                                                                                                                                                                                                                                                                                                        07-FEB-2001.
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Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 74
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain of sequences. (I) is useful as hybridisation probes, polymerase chain to reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in disgnostics as expressed sequence tags for identifying expressed of the disgnostics as expressed sequence tags for identifying expressed of sectivity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal cuplement (II) and its binding pattners are useful in medical imaging to polypeptide in tissue, as molecular weight markers and as a food of sites expressing (II). (I) and (II) are useful for treating disorders (Involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in colypeptide and polynucleotide sequences are applied and polynucleotide sequences or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cold sequences. AAS64197 AAS9454 represent novel human diagnostic colding sequences of the invention. Note: The sequence data for this cold sequences of the invention. Note: The sequence data for this cold sequences of the invention appear in the printed specification, but was obtained in the vivine way will be a sequences of the invention of manning and produced produ
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AAS72135 ID AAS72135 standard; cDNA; 2370

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13-FEB-2002 (first entry)

AAS72135;

us-09-436-184-3.oligo.rng

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The invention comprises the amino acid and coding sequences of proteins which have enzyme activity or protease, phosphodiesterase, transferase, or isomerase inhibitor activity. The DNA and protein sequences of the invention are useful for treating disorders associated with the proteins, such as blood clotting or circulatory disorders. The present DNA sequence represents a novel mouse gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protease inhibitors, proteases, phosphodiesterases, transferases, isomerases and substances that affect their activity or expression useful for treating associated disorders.
   novel protein; enzyme; blood clotting disorder; circulatory disorder; mouse; murine; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2803 BP; 546 A; 848 C; 854 G; 555 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; SEQ ID NO 15; 524pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y, Kamiya M, Kubodera H;
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30-APR-2002; 2002JP-00128657.
02-MAY-2002; 2002JP-00130918.
02-MAY-2002; 2002JP-00130918.
02-MAY-2002; 2002JP-00130918.
04-DEC-2002; 2002JP-0035236.
04-DEC-2002; 2002JP-00352559.
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(DNAF-) DNAFORM KK.
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Gaps ö 0.9%; Score 20; DB 12; Length 28 100.0%; Pred. No. 1.5e+02; Live 0; Mismatches 0; Indels Best Local Similarity 100. Matches 20; Conservative ò

Query Match

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2324; Conservative 0; Mismatches
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NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
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Batent No US20020110559A1
GENERAL INFORMATION:
GAPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
APPLICANT: Deutch, Alan H
APPLICANT: Glanbari, Hossein A
TITLE OF INVETION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REFERENCE: 21468-013 CIP
CURRENT FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 09/436,184
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TCATCTTTGATGACTCCTTTGAGCACGAGGTATGGCAGGATGCCTCATCTTTCCGGCTGA
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APPLICANT: Wands, Jack R.
APPLICANT: de la Monte, Suzanne M.
APPLICANT: Ince, Nedim
APPLICANT: Carlson, Rolin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REPRENCE: 21466-032 DIV3
CURRENT APPLICATION NUMBER: US/09/903,063
CURRENT APPLICATION NUMBER: US/09/903,063
CURRENT PILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 09/436,184
PRIOR PILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VE: 2.1
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; Patent No. US20020114810A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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 CURRENT APPLICATION NUMBER: US/09/903,216
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/436,184
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3.2
                                                                                                              Query Match
Best Local Similarity 100.
Matches 2324; Conservative
                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                   LENGTH: 2324
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APPLICANT: Carlson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: 21486-032 DIV.
CURRENT APPLICATION NUMBER: US/09/903,023
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 09/436,184
PRIOR APPLICATION NUMBER: 09/436,184
NUMBER OF SEQ ID NOS: 9
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SOFTWARE: PATENT NOS: 9
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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Sequence 3, Application US/09903023;
Patent No. US20020146421A1
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne M.
APPLICANT: Ince, Nedim

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241 TTGTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGGAG 300 301 ATTTGATGTGCATGATGCCAAAGTTTTATTAGGACTTAAAGAGATCTACTTCAGAGC 360 301 ATTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAGAGATCTACTTCAGAGC 360 361 CAGCAGTCCCGCCAGAAGATTTATTAGGACTTAAAGAGAAGATCTACTTCAGAGC 360 361 CAGCAGTCCCGCCAGAAGAGGCTGAGCCACACTGAGCCCGAGGAGCAGGTTCCTGTGG 420 421 AGGCAGAACCCCAGAATATCGAAGAAGAACAAAATACGAACCCTTCTCCATG 480 421 AGGCAGAACCCCAGAATATCGAAGAAAAGAACAAAATTCAGTCCTTCTCCATG 480	481 AAATGGTACACGCAGAACATGTTGAGGAGAAGACTTGCAACAAGAAGATGGACCCACAG 540 1	601 AGACCCTGGAACTGAGTATCTCATGAAGAAACCGAGCATACTTACCACGTGGAAGAGA 660 401 AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGA 660 601 AGACCCTGGAACCTGAATCAGGATATGAGAAGATGATGTCTGAGAGAGA	ATTCCAGTGAACCAGTAGTAGAAGATTGCACCATGATACAGTGATGATTACTTAC	901 AAGTAAGCATTTTCCTGTGGAAGAACAGGAAGTACCACCAGAAACAATTGAAAAA 900 901 AAGTAAGCATTTTCCTGTGGAAGAACAGCAGGAAGTACCACCAGAAACAATAGAAAAA 960 901 AAGTAAGCATTTTCCTGTGGAAGAACAACCAGGAAGTACCACCAGAAACAAATAGAAAAA 960 961 CAGATGATCCAGAACAAAAAGCAAAAGTTAAGAAAAAAAA	AAAGCTGAACTTGATGCTGCAGAAAAACTCCGTAAAAGGGGAAAAA AAAGCTGAACTTGATGCTGCAGAAAAACTCCGTAAAAGGGGAAAAA AATGCTGTAGTACGCAGAAAAACTCCGTAAAAGGGGAAAAA AATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAG	1141 CAAGATATGGGAAGGCGCAGTGTGAGATGATTTGGCTGAGAAGAGAGAG	1261 ACCTGCTGAAGCTGAGTTGAAGCGTCGGCCAGACAATTTCTAGGTCATATGA 1320
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" NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 089172.13
US-10-084-811-62
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APPLICANT: Sharon E. Plon
APPLICANT: Jason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REFERENCE: PA-0046 US
CURRENT APPLICATION NUMBER: US/10/084, B17
CURRENT FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/270, 784
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PERL PROGRAM
SEQ ID NO 63
LENGTH: 5358
                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                             DB 15;
                                                                                                                                                                                                                         Query Match 93.4%; Score 2171; DB 1
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2321; Conservative 0; Mismatches
                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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; Sequence 3, Application US/10269909
; Publication No. US20030180747A1
; GENERAL INFORMATION:
; APPLICANT: HRUBAN, RALPH H.
; APPLICANT: ARCHIVI, PEDRAM
; APPLICANT: ARCHIVI, PEDRAM
; APPLICANT: ARCHIVI, PEDRAM
; TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES
; TILLE REFERENCE: 58303 (71569)
; CURRENT APPLICATION NUMBER: US/10/269,909
; CURRENT APPLICATION NUMBER: 60/328,609
; PRIOR APPLICATION NUMBER: 60/328,609
; PRIOR APPLICATION NUMBER: 60/332,754
; RICH FILING DATE: 2001-110-11
; PRIOR APPLICATION NUMBER: 60/332,754
; RUMBER OF SEQ ID NOS: 87
; SOFTWARE: PALENTIN Ver. 2.1
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                                                    AAAACCTGAGGGAAAAAGGGGGACTGGAGCTCCAGGTGCGCTGCGAGGAAGAAGAA
                                                                                         ATGAAAATGCCTGCAAAGGAGCTCCTAAAACCTGTACCTTACTAGAAAAGTTCCCCGAGA
                                                                                                                                                            CAACAGGATGCAGAAGAGGACAGATCAAATATTCCATCATGCACCCGGGACTCACGTGT
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; Bedlication No. US20030166887A1
; GENERAL INFORMATION:
; APPLICANT: The Brigham and Women's Hospital, Inc.
; APPLICANT: Yates, Karen
; APPLICANT: Mizuno, Shuich;
; PILE REFERENCE: B0801/7244/KA/ERP
; CURRENT APPLICATION NUMBER: US/10/096,534
; CURRENT APPLICATION NUMBER: US 60/274,980
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: ALS680
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99.9%; Pred. No. 0;
cive 0; Mismatches
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; ORGANISM: Homo sapiens
US-10-096-534-37
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Score 640; DB
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                           Sequence 1791, Application US/09736457
Patent No. US20020168637A1
GENERAL INFORMATION:
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Best Local Similarity 99.9%;
Matches 690; Conservative
                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
          RESULT 11
US-09-736-457-1791
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US-09-736-457-1791
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                                              Length 2680;
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                                              DB 16;
                                             38.5%; Score 895; DB
llarity 99.9%; Pred. No. 0;
Conservative 0; Mismatches
; LENGTH: 2680
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-269-909-3
                                                     Similarity
                                            Query Match
Best Local Simil
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                                         526 AGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTATATCAGGATATGGATGATGATGATG
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                                                                                                                                                    GATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA
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                                                                                 TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGAAGATGAAAGATTGCACCAT
                                                                                                            586 TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCAT
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; Bublication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Bangur, Gary
; APPLICANT: Bangur, Gary
; APPLICANT: Wang, Aijun
; APPLICANT: Wang, Tongrong
; APPLICANT: Wang, Tongrong
; APPLICANT: Mune
; APPLICANT: Calapser, Anne
; APPLICANT: Calapser, Jonathan
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; TILE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; TILE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; TILE OF SEQ ID NOS: 1926
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT PILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FREEKSEQ for Windows Version 3.0
; SEQ ID NO 1791
LENGTH: 2442
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; Pred. No. 0;
0; Mismatches
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US-09-849-626-1791
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APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Darrick
APPLICANT: Ranger, Darrick
APPLICANT: Fanger, Thomas S.
APPLICANT: Fanger, Chaltanya S.
APPLICANT: McNabb, Andria
APPLICANT: McNabb, Andria
APPLICANT: McNabb, Andria
APPLICANT: Wondb, Andria
APPLICANT: WONDBD: 20121.478C17
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: UNMERR: US/09/902,941
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 2442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2442;
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99.9%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                  Sequence 1791, Application US/09902941
Patent No. US20020172952A1
GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
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CORGANISM: Homo sapiens
US-09-902-941-1791
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Best Local Similarity
                                                                                                                                                         RESULT 12
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| Sequence 1791, Application US/10113872
| Publication No. US20030170255A1
| Fabbication No. US20030170255A1
| APPLICANT: Watenabb. Yoshihiro
| APPLICANT: Henderson, Robert A. APPLICANT: Aleah, Michael D. APPLICANT: Stath, Paul R. APPLICANT: Carter, Darrick, Tommas S. APPLICANT: Carter, Darrick, Tommas S. APPLICANT: Carter, Darrick
| APPLICANT: Fanger, Gary R. TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER | TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER | TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER | TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER | TITLE OF INVENTION UNDBER: US/10/113,872
| CURRENT FILING DATE: 2002-03-28 | NUMBER OF SEQ ID NOS: 2011
| SEQ ID NO 1791
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US-10-113-872-1791
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406 CAAGAAGATGGACCCACAGAGAACCACAACAAGAGGATGATGAGTTTCTTATGGCGACT
                                                                 642 AGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGATGTG
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APPLICANT: Watenabe, Yoshihiro
APPLICANT: Watenabe, Yoshihiro
APPLICANT: Retrer, Marc W.
APPLICANT: Retrer, Marc W.
APPLICANT: Retrer, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Panger, Cary R.
APPLICANT: Panger, Cary R.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andrianya S.
APPLICANT: McNabb, Andrianya S.
APPLICANT: McNabb, Andrianya S.
APPLICANT: McNabb, Andrianya S.
APPLICANT: AND DIAGNOSIS OF LUNG CANCER
TITLE REPERENCE: 210121.478C18
CURRENT PILING DARE: 2004-10-29
CURRENT PILING DARE: 2004-10-29
SOFTWARE: FASC ID NOS: 2004
SOFTWARE: PASC ID NOS: 2004
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27.5%; Score 640; DB 14; Length 2442;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 690; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                             Sequence 1791, Application US/1001754
Publication No. US20030054363A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA; ORGANISM: Homo sapiens
US-10-017-754-1791
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                                                                                              ATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAA 521
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                    226 GAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCCTGAGCCACACACTGAGCCC
GAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGCCCACACTGAGCCC
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Sequence 1791,91, Application US/10283017
Sequence 1791,91, Application US/10283017
Senemal Information
APPLICANT: Henderson, Robert A.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Carter, Durham, Margarita
APPLICANT: Carter, Darrick
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Banger, Chaitanya S.
APPLICANT: Mandabb, Andaria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CURRENT FILLING DATE: 2002-10-28
NUMBER OF SEQ ID NOS: 2157
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1991
LENGTH: 2442
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9%;
Matches 690; Conservative C
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CRGANISM: Homo sapiens
US-10-283-017-1791
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162 GGAACTICATICTICACGIGGITIAIGGIGAITGCATIGCIGGGCGICIGGACAICTGIA 221

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                                                                  GCTGTCGTTTGGTTTGATCTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTAT
                                                                                         106 GCTGTCGTTTGGTTTGATCTTGTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTAT
                                                                                                                                                          282 GATGCTGATGGTGATGTTTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAA
                                                                                                                                                                                                                                                    GAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGCCCACACACTGAGCCC
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PREVENTION, AND
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhan
APPLICANT: Wengy Youzhan
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT, PREY
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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103

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1092 GIGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAGCAAGATATGGG 1151
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; Sequence 3202, Application US/0969034
; Publication No. US2004011068A1
; GENERAL INFORMATION:
    APPLICANT: Burgess, Christopher C.
    APPLICANT: Cariol, Theodore J.
    APPLICANT: Catino, Theodore J.
    APPLICANT: Catino, Theodore J.
    APPLICANT: Daivedi, Poornima
    APPLICANT: Thiagalipan, Arunthathi
    APPLICANT: Thiagalipan, Arunthathi
    APPLICANT: Thiagalipan, Arunthathi
    APPLICANT: Thiagalipan, Arunthathi
    APPLICANT: Molino, Gary A.
    APPLICANT: Lewis, Marcia E.
    TITLE OF INVENTION: Nucleic Acid Sequences Differentially
    TILLE OF INVENTION: Nucleic Acid Sequences
    TILLE OF INVENTION: Nucleic Acid Sequences
    TILLE OF INVENTION: Nucleic Acid Sequences
    TILLE OF INVENTION: Number: US/09/969,034
    TILLE OF INVENTION: UNMBER: 60/237,271
    PRIOR FILING DATE: 2000-10-02
    PRIOR FILING DATE: 2000-2-10
    NUMBER OF SEQ ID NOS: 4494
    SOFTWARE FEASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                      Length 502
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19.8%; Score 459; DB 10; I
Best Local Similarity 100.0%; Pred. No. 1.7e-226;
Matches 459; Conservative 0; Mismatches 0;
               PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 34279
LENGTH: 502
                                                                                                                                        YYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
COCATION: (1)...(502)
OTHER INFORMATION: n = A,T,C or G
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US-09-969-034-3202/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 AAAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGA 511
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                                                                                                                                                                                                                                                                                                                                                                                        Gaps
LOCATION: 3009, 3010, 3011, 3012, 3013, 3014, 3015, 3016, 3017, 3018, 20CATION: 3019, 3020, 3021, 3023, 3023, 3024, 3025, 3026, 3027, 3028, 2026, 3020, 3020, 3021, 3023, 3033, 3034, 3035, 3036, 3037, 3038, 2026, 3047, 3048, 3049, 3049, 3041, 3042, 3043, 3044, 3045, 3046, 3047, 3048, 3047, 3048, 3047, 3048, 3047, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3049, 3050, 3051, 3052, 3053, 3106, 3107, 3108, 3109, 3048, 3048, 3049, 3050, 3051, 3052, 3053, 3106, 3107, 3108, 3109, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048, 3048
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US-09-918-995-34279
US-09-918-995-34279
Sequence 34279, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
TTYLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: PROM VARIOUS CDNA LIBERARIES
TITLE OF INVENTION: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
                                                                                                                                                                                                                                                                                                                              Query Match 26.5%; Score 615; DB 14; L. Best Local Similarity 100.0%; Pred. No. 2.8e-307; Matches 615; Conservative 0; Mismatches 0;
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251 TGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGT
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Best Local Similarity 99.7%;
Matches 365; Conservative
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                                                                                                                                                                                                                                                                                                                     361 ACAAGA 366
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US-10-085-783A-25661
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| Sequence 25661. Application US/10242535A |
| Publication No. US20040013663A1 |
| GENERAL INFORMATION: Compositions and Methods Relating to Osteoarthritis |
| APPLICANT: ChondroGene Inc. |
| APPLICANT: ChondroGene Inc. |
| TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis |
| FILE REFERENCE: 4231/2005 |
| TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis |
| FILE REFERENCE: 4231/2005 |
| FILE REFERENCE: 4231/2005 |
| PRIOR APPLICATION NUMBER: US 10/085,783 |
| PRIOR APPLICATION NUMBER: US 60/275,017 |
| PRIOR FILING DATE: 2001-07-12 |
| PRIOR FILING DATE: 2001-03-12 |
| PRIOR FILING DATE: 2001-03-12 |
| PRIOR FILING DATE: 2001-02-28 |
| NUMBER OF SEQ ID NOS: 58994 |
| SOFTWARE: PatentIn version 3.2 |
| LENGTH: 366
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                                                                                                                                 Query Match 15.4%; Score 359; DB 11; Length 660; Best Local Similarity 100.0%; Pred. No. 1.1e-174; Matches 359; Conservative 0; Mismatches 0; Indels
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Pred. No. 6.4e-152;
0; Mismatches 1;
                                                               NAME/KEY: misc_feature;

// LOCATION: 507, 554, 599, 656

// OTHER INFORMATION: n = A,T,C or G

US-09-969-034-3202
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Best Local Similarity 99.7%;
Matches 365; Conservative (
       LENGTH: 660
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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US-10-085-783A-25661
US-10-085-2561, Application US/10085783A
US-10-085-2561, Application No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT PILING DATE: 2001-02-28
PRIOR PELLOR TOWNER: US 60/205,917
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR PILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patentin version 3.2
SEQ ID NO 25661
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                                                                        GGATGATGATGCCAAAGTTTTATTAGGACTTAAAAGAGAGATCTACTTCAGAGCCAGCAGTCCC
                                                                                                                              371 GCCACAGAGGCTGAGCCACACTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACC
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Gaps
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Pred. No. 6.4e-152;
0; Mismatches 1;
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; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-2707
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; ORGANISM: Human
US-10-085-783A-2707
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CGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAGGAGAACCCACA 550
                              GAAGAGATGATGTCTGAGCAGGAAAATCCAGATTCCAGTGAACCCAGTAGAAGATGAA 749
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| Publication No. US20030087918A1
| Publication No. US20030087918A1
| APPLICANT: Jiang Yuqiu
| APPLICANT: Jiang Yuqiu
| APPLICANT: Lodes, Michael J.
| APPLICANT: Lodes, Michael J.
| APPLICANT: Earger, Garrick
| APPLICANT: Seriet, Heacher
| APPLICANT: Seriet, Heacher
| APPLICANT: Sarick
| APPLICANT: Shith, Carole L.
| APPLICANT: Sarick
| APPLICANT: Sarick
| APPLICANT: Sarick
| APPLICANT: Sarick
| TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
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| TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
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LOCATION: 341, 343
SOTHER INFORMATION: n = A,T,C or G
US-10-066-543-277
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ORGANISM: Homo sapiens
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US-10-242-535A-2707
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APPLICANT: Liew, C.C.,
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT APPLICATION NUMBER: US/202-09-12
PRIOR FILING DATE: 2002-09-28
PRIOR FILING DATE: 2002-09-28
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR PLILOS DATE: 2001-03-12
PRIOR PLILOS DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
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APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REPERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
FRIOR APPLICATION NUMBER: US 60/305,340
FRIOR FILING DATE: 2001-07-13
FRIOR FILING DATE: 2001-07-13
FRIOR FILING DATE: 2001-07-13
FRIOR FILING DATE: 2001-03-12
FRIOR FILING DATE: 2001-03-12
FRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PREENTIN VERSION 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 5.8%; Score 135; DB 17; Best Local Similarity 100.0%; Pred. No. 1.1e-58; Matches 135; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 5.8%; Score 135; DB 17; Best Local Similarity 100.0%; Pred. No. 1.1e-58; Matches 135; Conservative 0; Mismatches 0;
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; Sequence 2707, Application US/10085783A
; Deblication No. US20040037841A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               487 TACACGCAGAACATG 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INCOMPATION:

GENERAL INCOMPATION:

GENERAL INCOMPATION:

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2002-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-24

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-08-08

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOSTWARE PACKSEQ FOR WINGOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                          162 GGAACTTCATTCTTCACGTGGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTA
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Sequence 2865, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108027.129
CURRENT APPLICATION NUMBER: US/10/027,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                       Length 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 GCTGTCGTTTGGTTTGATCTTGACTATGAGGAAGTTCTAGG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OLHER INFORMATION: SWISSPROT HIT: Q12797, EVALUE 3.00e-14; OTHER INFORWATION: NT HIT: G114589865, EVALUE 2.00e-80
US-10-029-386-13264
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                           4.5%; Score 104; DB 16; 100.0%; Pred. No. 1.3e-42; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
3.4%; Score 78; DB 13; I
Best Local Similarity 100.0%; Pred. No. 3.7e-29;
Matches 78; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2825, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
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                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 28
US-10-027-632-2825/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-027-632-2825/c
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US-10-027-632-2825
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SEQ ID NO 2825
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Publication No. US2030194704A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, DAVID R.
APPLICANT: ABOMICA-X-2
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
LENGTH: 592
LENGTH: 592
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26964, Application US/10029386

| Sequence 26964, Application US/10029386
| Publication No. US2030194704A1
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G.
| APPLICANT: Penn, David R.
| APPLICANT: Hanzel, David R.
| APPLICANT: Hanzel, David R.
| TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
| TITLE OF INVENTION ANALYSIS TWO
| TITLE OF INVENTION ANALYSIS TWO
| TITLE OF INVENTIO
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                                               61 AACCCCAGAATATCGAAGATGAAGCAAAAAAAAAAATTCAGTCCCTTCTCCATGAAATGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EST_HUMAN HIT: AU132666.1, EVALUE 4.00e-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: MAP TO CHR8.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED THT: Q12797, EVALUE 4.00e-15
OTHER INFORMATION: EST HUMAN HIT: AW87165.1, EVALUE 9.00e-81
OTHER INFORMATION: NT HIT: 9114589861, EVALUE 6.00e-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-42; Matches 104; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 GCTGTCGTTTGGTTTGATCTTGACTATGAGGAAGTTCTAGG 265
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                                                                                                                                                                                                                           487 TACACGCAGAACATG 501
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                          RESULT 25
US-10-029-386-26964/c
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RESULT 30
US-09-908-975-11070

Sequence 11070, Application US/09908975

PUBLICATION NO. US20030165843A1

SEQUENCE 11070, Application US/09908975

PUBLICATION NO. US20030165843A1

APPLICANT: MINTZ, E1,

CURRENT: FAIGLER, Simchon

TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE

TITLE OF INVENTION: UNMER: US/09/908,975

CURRENT FILING DATE: 2001-07-20

PRIOR PELICATION NUMBER: US 60/287,724

PRIOR PELICATION NUMBER: US 60/287,724

PRIOR PILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 32337

SOFTWARE: PATENTING OFFERE 
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Publication No US20030211476A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Branceutical Technology
APPLICANT: Branchon, Daniel J.
APPLICANT: Branchon, Daniel J.
APPLICANT: Branchon, Daniel J.
APPLICANT: Branchin, Imelda
APPLICANT: Jambin, Imelda
APPLICANT: Haghin, Imelda
APPLICANT: Haghin, Insa
ITILE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: E1067/20087
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2239 GGCATCCGGAACTGACACACAGAGAGACGCCTTCCAGCAATTTAGCATGAATTC 2297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAATCCAGATTCCAGTGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 GECATCCGGAACTGACACCACAGCAGAGACGCAGCCTTCCAGCAATTTAGCATGAATTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Best Local Similarity 100.0%; Pred. No. 7.3e-20;
Matches 60; Conservative 0; Mismatches 0;
                        293 AGTTTTATTAGG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-275-322
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US-10-116-275-322/c
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LENGTH: 2208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 AGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 AGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGTGGTGATGCCAA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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Best Local Similarity 100.0%; Pred. No. 3.7e-29;
Matches 78; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/10443622

Publication No. US20040024192A1
GENERAL INFORMATION:
APPLICANT: Carter et al.
ITILE OF INVENTION: 19 Human Secreted Proteins
FILE REFERENCE: P2009P1
CURRENT APPLICATION NUMBER: US/10/443,622
CURRENT APPLICATION NUMBER: US/10/443,622
CURRENT APPLICATION NUMBER: US/05/13608
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
PRIOR PLILING DATE: 1997-07-01
PRIOR APPLICATION NUMBER: 60/051,381
PRIOR APPLICATION NUMBER: 60/058,663
PRIOR APPLICATION NUMBER: 60/058,663
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 156
SOFTWARE: Patentin Ver: 2.0
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/165,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: US 60/166,002
PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409 AGGITCCIGTGGAGGCAG 426
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CORGANISM: Homo sapiens
US-10-443-622-24
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; ORGANISM: Human
US-10-027-632-2825
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TYPE: DNA
ORGANISM: Human
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        Sequence 177, Application US/10755889

Sequence 177, Application US/20040171823A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: PATHWAX
FILE REFERENCE: DO244 NP

CURRENT APPLICATION NUMBER: US/10/755,889

CURRENT FILING DATE: 2004-01-13

PRIOR PRILING DATE: 2003-01-14

PRIOR PILING DATE: 2003-05-12

NUMBER OF SEQ ID NOS: 823

SOFTWARE: Patentin version 3.2

SEQ ID NO 177

LENGTH: 2008
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| GENERAL INFORMATION: | APPLICANT | |
| APPLICANT | AGELE, Jon H. |
| APPLICANT | Carroll, Eddie III |
| APPLICANT | Carroll, Eddie III |
| APPLICANT | Cariol, Theodore J. |
| APPLICANT | Daivedi | Pocnima |
| APPLICANT | Thiagalingam, Arunthathi |
| FILE REFERENCE | 1657/1032 |
| CURRENT FILING DATE: 2001-00.2 |
| PRIOR FILING DATE: 2000-02-10 |
| PRIOR PILING DATE: 2000-02-10 |
| PRIOR FILING DATE: 2000-02-10 |
| NUMBER OF SEQ ID NOS: 4494 |
| SOFTWARE: FREESEQ for Windows Version 4.0 |
| LENGTH: SB3 |
| LENGTH: SB
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2.2%; Score 51; DB 11; I
Best Local Similarity 100.0%; Pred. No. 3.7e-15;
Matches 51; Conservative 0; Mismatches 0;
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Pred. No. 2.8e-19;
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; LOCATION: 503, 512, 553, 565, 570, 577, 578
; COTHER INFORMATION: n = A,T,C or G
US-09-969-034-3266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3266, Application US/09969034
Publication No. US20040110668A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
US-10-755-889-177
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US-10-755-889-177/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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Sequence 1020, Application US/10027632

Publication No. US200019337A4

Publication No. US200019337A4

Publication No. US200019337A4

Publication No. US200019337A4

PUBLICATION WINDERS 10827.132

PRIOR PAPLICATION NUMBER: US 60/128,066

PRIOR PAPLICATION NUMBER: US 60/128,188

PRIOR
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us-09-436-184-3.oligo.rnpb

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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 310460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 39
US-10-027-632-310460/c
Sequence 310460, Application US/10027632
Publication No. US20030204075A9
GENERAL INFERMATION:
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Best Local Similarity 100.
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39; Conservative
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Matches 39; Conserv
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US-10-027-632-56205/c
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US-10-027-632-310460
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; ORGANISM: Human
US-10-027-632-56205
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Sequence 55205, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPERBNCE: 108627.123

CURRENT FILING DATE: 2002-04-30

FRIOR APPLICATION NUMBER: US 60/18,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PLING DATE: 2000-04-20

PRIOR PLING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PLING DATE: 1999-10-23

PRIOR PLING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 325720-

SOFTWARE: FESSEE SEC FOR WINGOWS VERSION 4.0

SEQ ID NO 56205

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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR PLILNG DATE: 2000-07-12

PRIOR PLILNG DATE: 2000-07-12

PRIOR PLILNG DATE: 2000-04-20

PRIOR PLILNG DATE: 2000-04-20

PRIOR PLILNG DATE: 2000-03-29

PRIOR PLILNG DATE: 2000-03-24

PRIOR PLILNG DATE: 2000-03-24
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                                                               Query Match
1.9%; Score 44; DB 17; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 44; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 6e-09;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               304 AGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCACAG 347
                                                                                                                                                                                                                        800 AGCAGTATATGAACCTCTAGAAATGAAGGGATAGAAATCACAG 843
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Sequence 310460, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
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Best Local Similarity 100.0

Matches 39; Conservative
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US-10-027-632-56205/c
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-027-632-56205
US-10-027-632-7020
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Sequence 56205, Application US/10027632

Sequence 56205, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

ITTLE OF INVENTION: Identification and Mapping of Single Nucleotide

ITTLE OP INVENTION: Delymorphisms in the Human Genome

FILE REFERENCE: 10827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04.30

FRIOR APPLICATION NUMBER: US 60/18,006

FRIOR APPLICATION NUMBER: US 60/198,676

FRIOR PELING DATE: 2000-04-20

FRIOR PELING DATE: 2000-04-20

FRIOR FILING DATE: 2000-04-20

FRIOR PILING DATE: 2000-03-24

FRIOR PILING DATE: 1000-03-24

FRIOR PILING DATE: 1000-03-24

FRIOR PILING DATE: 1009-03-28

FRIOR PILING DATE: 1999-01-23

FRIOR APPLICATION NUMBER: US 60/166,358

FRIOR PILING DATE: 1999-01-83

FRIOR APPLICATION NUMBER: US 60/166,368

FRIOR PILING DATE: 1999-01-83

FRIOR APPLICATION NUMBER: US 60/166,368

FRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SECPTAMER: PREAUSEQ for Windows Version 4.0
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   Length 453;
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100.0%; Pred. No. 6e-09;
tive 0; Mismatches 0; Indels
                                                                    0; Indels
                                                                                                                                                                      453 CTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGC 415
                                                                                                                                  349 CTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGC 387
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1.7%; Score 39; DB 13;
100.0%; Pred. No. 6e-09;
iive 0; Mismatches 0
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/437,963 .
CURRENT APPLICATION NUMBER: US/10/437,963 .
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 73067
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APPLICANT: Rovalic, David K.
APPLICANT: Thou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(53222)
CURRENT APPLICATION NUMBER: US/10/425,115
                TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REPERBRUE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 124491
LENGTH: 2135
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100.0%; Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                            DB 18;
1.2;
                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Clone ID: MRT4577_45013C.1
US-10-425-115-124491
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Best Local Similarity 100.0%; Pred. No. -...
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                         / Match 1.0%; Score 23; DB Local Similarity 100.0%; Pred. No. 1.3 nes 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1991 GCAGCGCCAACAGCAGCAGCAGC 1969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42949, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 73067, Application US/10437963
Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                     37 GCAGCGGCAACAGCAGCAGCAGC 59
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         Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-425-115-42949/c
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                                                                                                                                                                                                                                                          FEATURE:
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Matches
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US-10-424-599-97119

Sequence 97119, Application US/10424599

Sequence 97119, Application US/10424599

Publication No. USCO040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(55223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 97119
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100.0%; Pred. No. 0.36;
tive 0; Mismatches 0; Indels
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US-10-424-599-97119
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Pred. No. 6e-09;
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-08-28
PRIOR PILING DATE: 1999-08-28
PRIOR PILING DATE: 1999-08-28
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEC ID NOS: 325720
SEC ID NO 310460
LENGTH: 453
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Best Local Similarity
Matches 39; Conserva'
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US-10-425-115-124491/c
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APPLICANT: Wands, Jack R.
APPLICANT: Deutch, Alan H
APPLICANT: Ge la Monte, Suzanne M
APPLICANT: Ghanbari, Hossein A
ITILE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REFERENCE: 21466-032 CIP
CURRENT APPLICATION NUMBER: US/09/859,604
CURRENT FILING DATE: 2001-05-17
FRIOR APPLICATION NUMBER: 09/436,184
FRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 11
                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:Location (-1); OTHER INFORMATION: Oligonucleotide US-09-859-604-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:Location (-6) OTHER INFORMATION: oligonucleotide
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APPLICANT: Wands, Jack R.
APPLICANT: de la Monte, Suzanne M
APPLICANT: de la Monte, Alan H
APPLICANT: de la Monte, Alan H
APPLICANT: Ghanbari, Hossein A
TITLE.OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
TITLE.OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
CURRENT APPLICATION NUMBER: US/09/859,604
PRIOR APPLICATION NUMBER: 09/436,184
PRIOR PILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 13
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37;
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   PRIOR APPLICATION NUMBER: 09/436,184
PRIOR FILING DATE: 1999-11.08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09859604; Patent No. US20020110559A1; GENERAL INFORMATION:
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US-09-859-604-12/c
; Sequence 12, Application US/09859604
; Patent No. US20020110559A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AATGGCCCAGCGTAAGAATG 30
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                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-859-604-11/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-859-604-11
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US-10-308-503-188
Sequence 188, Application US/10308503
Sequence 188, Application US/10308503
Sequence 188, Application US/10308503
Sequence 188, Application No. US20030191080A1
SEQUENCE INFORMATION: ANTIENDE COMPOSITIONS TARGETED TO BETA1-ADRENOCEPTOR-SPECIFIC MR
TITLE OF INVENTION: ANTIENDES OF USE
FILE REPERENCE: 4300-013900
CURRENT FILING DATE: 2003-12-03
SPRIOR APPLICATION NUMBER: US/10/308,503
CURRENT FILING DATE: 2000-07-11
PRIOR FILING DATE: 1998-09-14
SPRIOR FILING DATE: 1998-09-14
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GENERAL NEORMATION:
APPLICANT: Wands, Jack R.
APPLICANT: Ge la Monte, Suzanne M
APPLICANT: Ghanbari, Hossein A
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REFERENCE: 21486-032 CIP
CURRENT APPLICATION UNMER: US/09/859,604
CURRENT FILING DATE: 2001-05-17
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                                                                                                                                                                                                                                                                                                      Query Match 0.9%; Score 21; DB 18; Length 715; Best Local Similarity 100.0%; Pred. No. 13; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: MRT4577_139178C.1
US-10-425-115-42949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (1828)...(1828)
SOTHER INFORMATION: WHERE N = A, T, C OR G
US-10-308-503-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  462 GCGCAACAGCAGCAGCG 442
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 42949
LENCTH: 715
                                                                                                                         TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                    FEATURE:
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Ouery Match
Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-767-701-26002/c
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Sequence 21348, Application No. US20040214272A1

Sequence 21348, Application No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(53222)B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 21348
LENGTH: 183
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Sequence 22449, Application US/10425115
Sequence 22449, Application US/10425115
Sequence 22449, Application US/10425115
SEQUENCE 2240, Sequence 2240, Young Yo
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                                                                                                                                                                                      FEATURE:
COTHER INFORMATION: Description of Artificial Sequence:Locations (-11)
COTHER INFORMATION: 011gonucleotide
US-09-859-604-12
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100.0%; Pred. No. 40;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                         Length 20;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.9%; Score 20; DB 9; Best Local Similarity 100.0%; Pred. No. 37; Matches 20; Conservative 0; Mismatches (
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US-10-425-115-21348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 cggaccgrccaarggcccag 1
                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Zea mays
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US-10-425-115-21348/c
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US-10-425-115-22449
                                        SEQ ID NO 12
LENGTH: 20
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Sequence 89196, Application US/10424599

Sequence 89196, Application Wo. US2004031072A1

Sequence 89196, Application Wo. US2004031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 89196
SEQ ID NO 89196

LENGTH: 495
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cabo, Yongwa K.
APPLICANT: Cabo, Yongwa K.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
SEQ ID NO 26602
LENGTH: 489
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                                                        Indels
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US-10-424-599-89196
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OTHER INFORMATION: unsure at all n locations
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Query Match 0.9%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 41; Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                              Sequence 26002, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
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US-10-767-701-26002
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                                                                                                                40 GCGCCAACAGCAGCAGCAGC 59
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USERIOR 22022, Application US/10027632

| Sequence 322022, Application US/10027632
| Publication No. US20020198371A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Dolymorphisms in the Human Genome
| FILE REFERENCE: 108827.129
| PRIOR FILING DATE: 2000-07-12
| PRIOR FILING DATE: 2000-07-29
| PRIOR FILING DATE: 2000-03-29
| PRIOR FILING DATE: 2000-03-29
| PRIOR FILING DATE: 2000-02-24
| PRIOR FILING DATE: 1200-02-24
| PRIOR FILING DATE: 1200-02-24
| PRIOR FILING DATE: 1999-10-23
| PRIOR FILING DATE: 1999-09-28
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US-10-027-632-322023/c

Sequence 322023, Application US/10027632

Publication No. US2020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPERENCE: 108927.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT PILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PILING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-24
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                                                                                                                  DB 13; Length 567;
42;
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100.0%; Pred. No. 42;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                    0; Indels
                                                                                                                      Query Match 0.9%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 42; Bettches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                 972 GAACAAAAGCAAAAGTTAA 991
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Best Local Similarity 100.
Matches 20; Conservative
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; ORGANISM: Human
US-10-027-632-322022
    ; ORGANISM: Human
US-10-027-632-82527
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                                                                                                                                                                                      Sequence 9144, Application US/10029386
Sequence 9144, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CTITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ.ID NOS: 34288
SSEQ ID NO 9144
LENGTH: 550
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Sequence 8227, Application US/10027632

Publication No. US20020198371A1

SERVERAL INFORMATION:
INFORMATION:
APPLICANT: Wang, David G.
ITILE OF INVENTION: Polymorphisms in the Human Genome
ITILE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-04-20
PRIOR PRIOR DATE: 2000-04-20
PRIOR PRIOR OF INVENTION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-02-29
PRIOR PRIOR DATE: 2000-02-29
PRIOR PRIOR DATE: 2000-02-29
PRIOR PRIING DATE: 1000-02-29
PRIOR PRIING DATE: 1000-02-24
PRIOR PILING DATE: 1000-02-24
PRIOR PRIING DATE: 1000-02-24
PRIOR PILING DATE: 1000-02-24
PRIOR PILING DATE: 1999-09-18
PRIOR PRIING DATE: 1999-09-28
PRIOR PRIING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
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OTHER INFORMATION: MAP TO AC007262.4

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN BEALM, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

OTHER INFORMATION: SMISSPROT HIT: P54258, EVALUE 1.80e+00

OTHER INFORMATION: WT HIT: AB051488.1, EVALUE 0.00e+00

OTHER INFORMATION: EST_HUMAN HIT: B1458804.1, EVALUE 7.00e-63

US-10-029-386-9144
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402 AGAAAAAGCCTAAACTT 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
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US-10-027-632-82527/c
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
CURRENT FILING DATE: 2002-04-30
PRIOR PLICATION NUMBER: US 60/198,676
PRIOR PLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR PLICATION NUMBER: US 60/185,218
PRIOR PLICATION NUMBER: US 60/186,368
PRIOR FILING DATE: 1999-11-23
PRIOR PLICATION NUMBER: US 60/166,368
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR PLICATION NUMBER: US 60/146,002
PRIOR PLICATION NUMBER: US 60/146,002
PRIOR PLING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FEALSEQ for Windows Version 4.0
SEQ ID NO 322023
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42;
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42;
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100.0%; Pred. No. -...
                       CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PLILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASESEQ FOR WINGOWS VERSION 4.0
SEQ ID NO 322022
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Best Local Similarity 100.0%; Pi
Matches 20; Conservative 0;
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Best Local Similarity 100.
Matches 20; Conservative
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US-10-027-632-322023
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US-10-027-632-322022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Tedentification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION WUMBER: US 60/218,006
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR PILING DATE: 2000-09-20
FRIOR PELING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-09-28
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR FILING DATE: 1999-09-08-09
FRIOR FILING DATE: 1999-09-08-09
FRIOR FILING DATE: 1999-09-08-09
FRIOR FILING DATE: 1999-08-09
FRIOR APPLICATION NUMBER: US 60/146,002
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100.0%; Pred. No. 42;
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PRIOR PLING DATE: 1999-11-23
PRIOR FLING DATE: 1999-09-28
PRIOR FLING DATE: 1999-08-09
PRIOR FLING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastesEQ for Windows Version 4.0
SEQ ID NO 322023
LENGTH: 567
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Publication No. US20030204075A9
GENERAL INFORMATION:
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Publication No. US20030204075A9
GENERAL INFORMATION:
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Best Local Similarity luv...
Best 20; Conservative
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Matches 20; Conserv
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US-10-027-632-322022/c
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US-10-027-632-82527/c
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ORGANISM: Human
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ORGANISM: Human
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; Sequence 1, Application US/10822613
; Publication No. US2005002905A1
; GENERAL INFORMATION:
; APPLICANT: SCARPACE, PHILIP J.
; APPLICANT: LI, GANG
; TITLE OF INVENTION: RAAV VECTOR-BASED PRO-OPIOMELANCORTIN COMPOSITIONS AND METHODS
; TITLE OF INVENTION: DF USE
; FILE REPERENCE: 4300.01540
; CURRENT APPLICATION NUMBER: US/10/822,613
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: 60/462,496
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 54
; SCFWARE: PatentIn Version 3.2
; SEQ ID NO 1
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Home sapiens
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 24406
LENGTH: 843
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US-10-437-963-24406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24466, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
APPLICANT: Wwi
APPLICANT: Bukharov, Andrey A.
APPLICANT: Barbayuk, Brad
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APPLICANT: La Rosa, Thomas J. APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Zhou, Yihua
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ORGANISM: Oryza sativa
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; Publication NG 20040123343A1
; Publication NG 2020040123343A1
; Publication NG US20040123343A1
; Publication NG US20040123343A1
; Publicant: La Rosa, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
; APPLICANT: Brabazuk, Brad
; APPLICANT: Lang OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TURENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 71261
; PUBLICANT: 771
                                                                                                                                         Sequence 112661, Application US/10425115
Publication Wo. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-4-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 112661
LENGTH: 750
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US-10-437-963-71261
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; OTHER INFORMATION: Clone ID: MRT4577_34237C.1
US-10-425-115-112661
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            212 GAACAAAAGCAAAAGTTAA 193
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ORGANISM: Zea mays
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US-10-822-613-1
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Suppression of the NURR
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Applicant: Active the construction of the const
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Patent No. US20020049151A1

GENERAL INFORMATION

APPLICANT: Murphy, Evelyn

APPLICANT: Conneely, Orla

APPLICANT: Etzgerald, Orlave

TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppressi

TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors

TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors

FILE REFRENCE: P01972US1

CURRENT APPLICATION NUMBER: US/09/853,386

CURRENT FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: US 60/203645

PRIOR FILING DATE: 2000-05-12

NUMBER OF SEQ ID NOS: 153

SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: MRT4577_96234C.1
US-10-425-115-180542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: PZ027P1
CURRENT APPLICATION NUMBER: US/09/397,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(1011)
OTHER INFORMATION: unsure at all n locations
FEATURE:
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; Sequence 80, Application US/09397945
; Publication No. US20030065139A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 AGCAGCAGCGCTCCGGCAG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 GCAACAGCAGCAGCAGCGGC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AGCAGCAGCGGCTCCGGCAG 70
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Best Local Similarity 100.
Matches 20; Conservative
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Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
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; ORGANISM: HUMAN
US-09-853-386-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 105
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          엄
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                                                                                                                              APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 51503
LENGTH: 924
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0.9%; Score 20; DB 18; Length 924;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Clone ID: PAT_MRT4530_53889C.1
US-10-437-963-51503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-1U-0940-02/04-08

Publication No. US20040138115A1

GENERAL INFORMATION

APPLICANT: WITTIG, Burghardt

APPLICANT: STHEIN, Christoph

APPLICANT: SCHAEFER, Matchael

APPLICANT: SCHAEFER, Matchael

APPLICANT: SCHROFF, Matthias

APPLICANT: CRENT MATHOR MERBIZ, Sven A.

TITLE REFERENCE: NHL-NP-43

FILE REFERENCE: NHL-NP-43

CURRENT FILING DATE: 2003-08-22

FRIOR APPLICATION NUMBER: DE 101 09 092.7

FRIOR APPLICATION NUMBER: DE 101 09 092.7

FRIOR FILING DATE: 2002-02-19

FRIOR FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 8: SEQ ID NOS: 10

LENGTH: 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.9%; Score 20; DB 18; Best Local Similarity 100.0%; Pred. No. 42; Matches 20; Conservative 0; Mismatches 0
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LOCATION: (847)...(933)
CTHER INFORMATION: beta-endorphin cDNA sequence
US-10-646-620A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 180542, Application US/10425115
Publication No. US20040214272A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       663 GCGCCAACACCACCACCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 GCGGCAACAGCAGCAGC 59
                                    Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
          Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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US-10-646-620A-8
                                           APPLICANT:
APPLICANT:
APPLICANT:
             APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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RESCULT.

Sequence 37, Application US/10287971

Sequence 37, Application US/10287971

Publication No. US20040067882A1

Publication No. US20040067882A1

SERVERAL INFORMATION:
THEAD TABODROOK, et al.

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REFERENCE: 21402-460A

CURRENT APPLICATION NUMBER: US/10/287,971

CURRENT FILING DATE: 2002-11-05

PRIOR APPLICATION NUMBER: US/957,425

PRIOR PELING DATE: 2001-11-29

PRIOR PELING DATE: 2001-11-29

PRIOR PELING DATE: 2001-11-05

PRIOR PELING DATE: 2001-10-05

PRIOR PELING DATE: 2001-11-05

PRIOR PELING DATE: 2001-11-06

PRIOR PELING DATE: 2001-11-09

PRIOR PELING DATE: 2001-11-09

PRIOR PELING DATE: 2001-11-09

PRIOR PELING DATE: 2001-11-09

PRIOR PELING DATE: 2001-11-09
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US-09-560-288-1
US-09-560-288-1
US-09-560-288-1
Sequence 1, Application US/09960288
Patent No. USZ002006483341
GENERAL INFORMATION:
APPLICANT: Pagerlund, Tore
APPLICANT: Alsetron, Perer
APPLICANT: Alsetron, Perer
FILE DF INVENTION: Recombinant plasmids and method for treating substance abuse
CURRENT APPLICATION NUMBER: US/09/960,288
CURRENT FILING DAFE: 1999-10-26
FRICR FILE APPLICATION NUMBER: 09/426,877
PROR APPLICATION NUMBER: 09/426,877
PROR APPLICATION NUMBER: 09/426,877
PROR PROR FILE NOS: 2
SOUTWARE: PatentIn version 3.0
SOUTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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   PRIOR FILING DATE: 1998-03-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 400
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 1109
TYPE: DDA
TYPE: DDA
ORGANISM: Homo sapiens
US-10-653-595-80
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                                                                                                                                                                                                                                                                                                                         Query Match 0.9%; Score 20; DB 17; Length 1109; Best Local Similarity 100.0%; Pred. No. 43; Matches 20; Conservative 0; Mismatches 0; Indels (
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0.9%; Score 20; DB 9; Length 1230;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 GCAACAGCAGCAGCAGCGGC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 GCAACAGCAGCAGCGGC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CRGANISM: Homo sapiens
US-09-960-288-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-653-595-80/C

US-10-653-595-80/C

PUBLICATION NO. US20040048304A1

GENERAL INFORMATION:

APPLICATION NO. US20040048304A1

APPLICATION NO. US20040048304A1

FILE OF INVENTION:

CURRENT FAPPLICATION NUMBER: US/10/653,595

CURRENT FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: US/9/97945

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: C0/078,566

PRIOR PILING DATE: 1999-03-19

PRIOR FILING DATE: 1998-03-19

PRIOR APPLICATION NUMBER: 60/078,574

PRIOR FILING DATE: 1998-03-19

PRIOR APPLICATION NUMBER: 60/078,574

PRIOR FILING DATE: 1998-03-19

PRIOR APPLICATION NUMBER: 60/078,574

PRIOR FILING DATE: 1998-03-19

PRIOR PILING DATE: 1998-03-19

PRIOR FILING DATE: 1998-04-01

PRIOR FILING DATE: 1998-04-01
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/078,56
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR PILING DATE: 1998-03-19
PRIOR PILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR PILING DATE: 1998-04-01
NUMBER OF SEQ. ID NOS: 470
ENGURTH: 110-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-09-397-945-80
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US-10-653-595-80/c
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TYPE: DNA
ORGANISM: Homo sapiens
       LENGTH: 1435
TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-10-425-114-34740/c
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabasks, Jack E
APPLICANT: Tabasks, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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Sequence 19062, Application US/10425115

Sequence 19062, Application US/10425115

Sequence 19062, Application US/10425115

Sequence 19062, Application US/0040214272A1

SEMENAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Number: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 19062
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100.0%; Pred. No. 43;
tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                     Query Match 0.9%; Score 20; DB 17; Length 1245; Best Local Similarity 100.0%; Pred. No. 43; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: LIB3599-031-D8_FLI
US-10-425-114-23644
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/406,181
PRIOR FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 397
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 37
LENGTH: 1245
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 23644, Application US/10425114; Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 GCAACAGCAGCAGCAGCGGC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    562 GCGGCAACAGCAGCAGCAGC 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                                                                                                                                                                                           ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (90)..(1091)
US-10-287-971-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 20; Conserve
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LENGTH: 1282
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APPLICANT: ALE GOVERNMENT OF THE UNITED STATES OF AMERICA AS APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND APPLICANT: HUMAN SERVICES APPLICANT: BEJAND, Kristi APPLICANT: Egland, Kristi APPLICANT: Lee, Byungkook APPLICANT: Lee, Byungkook APPLICANT: Vincent, James TITLE OF INVENTION: GENE EXPRESSED IN BREAST CANCER AND METHODS OF USE TITLE OF INVENTION: GENE EXPRESSED IN BREAST CANCER AND METHODS OF USE CURRENT APPLICATION NUMBER: US 10/10/913,196 CURRENT ELLING DATE: 2004-08-05 PRIOR FILING DATE: 2004-08-05 PRIOR FILING DATE: 2003-08-08 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin version 3.2 LENGTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kowalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Subject Screen, S
                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                Length 1435;
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                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                18;
; OTHER INFORMATION: Clone ID: MRT4577_117387C.1
US-10-425-115-19062
                                                                                                                                                              Query Match 0.9%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 43; Matches 20; Conservative 0; Mismatches
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Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   1908 CAAGGAAGAAGAATGAAA 1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1218 CAAGGAAGAAGAAATGAAAA 1237
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Publication No. US20050053988A1
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Best Local Similarity 100.0%; Pr
Matches 20; Conservative 0;
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0.9%; Score 20; DB 17; Length 1891;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels (
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (193)..(1380)
; OTHER INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT PILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 280
LENGTH: 1891
                                                                            Query Match 0.9%; Score 20; DB 17; Length 1850; Best Local Similarity 100.0%; Pred. No. 44; Matches 20; Conservative 0; Mismatches 0; Indels C
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17307H04_FLI
US-10-425-114-34740
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US-10-154-280
US-10-154-280
Publication No. US20030233670A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Edgerton, Michael D
APPLICANT: Adams, Thomas H
APPLICANT: Adams, Thomas H
APPLICANT: Adams, Jaffrey E.
APPLICANT: Ball, James A.
APPLICANT: Ball, Sanu, G.
APPLICANT: Ball, Sanu, G.
APPLICANT: Bell, Erin
APPLICANT: Bell, Stephan M.
APPLICANT: Bell, Stephan M.
APPLICANT: Huang, Shibshieh
APPLICANT: Lee, Gary
APPLICANT: Lee, Gary
APPLICANT: Luethy, Michael M.
APPLICANT: Luuthen, Adrian
APPLICANT: Luuthen, Adrian
APPLICANT: Madson, Linda L.
APPLICANT: Huang, Charchigh
APPLICANT: Parnell, Laurence D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Wang, Halyun
APPLICANT: Wang, Chunzhi
APPLICANT: Zhang, Qiang
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ORGANISM: Oryza sativa
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: March 25, 2005, 17:12:50 ; Search time 408 Seconds (without alignments)	ct score: 2324 nce: 1. cggaccgtgcaatggcccag ng table: OLIGO_NUC Gapop_60.0 , Gapext 60.0 hed: 1202784 seqs, 818138359 res	Inits satisfying chosen parameters: 2405568 length: 200000000 g: Listing first 100 summaries Issued_Patents NA:* 1: /cgn2_6/ptodata1/ina/5B_COMB.seq:* 2: /cgn2_6/ptodata1/ina/6B_COMB.seq:* 3: /cgn2_6/ptodata1/ina/6B_COMB.seq:* 5: /cgn2_6/ptodata1/ina/6B_COMB.seq:* 5: /cgn2_6/ptodata1/ina/PGTUS COMB.seq:* 6: /cgn2_6/ptodata1/ina/PGTUS COMB.seq:* 6: /cgn2_6/ptodata1/ina/PGTUS COMB.seq:* 6: /cgn2_6/ptodata1/ina/PGTUS COMB.seq:* 6: /cgn2_6/ptodata1/ina/Packfiles1.seq:* 7: /cgn2_6/ptod	2224 100.0 2324 4 US.09-903-248-3 2324 100.0 2324 4 US.09-903-248-3 2324 100.0 2324 4 US.09-903-216-3 2324 100.0 2324 4 US.09-903-16-3 232 10.0 2324 4 US.09-103-1791 640 27.5 2442 4 US.09-65-735-1791 640 27.5 2442 4 US.09-65-521-1 115 49 956 4 US.09-949-016-16189 115 49 956 4 US.09-949-016-122372 77 3.3 601 4 US.09-949-016-132387 78 3.3 601 4 US.09-949-016-132387 79 19 601 4 US.09-949-016-132387 20 0.9 324 4 US.09-949-016-132387 20 0.9 324 4 US.09-949-016-132387 20 0.9 324 4 US.09-859-604-10 20 0.9 324 4 US.09-859-604-12 20 0.9 324 4 US.09-859-604-13 20 0.9 1071 4 US.09-949-016-132387 20 0.9 1071 4 US.09-949-016-132387 20 0.9 1071 4 US.09-949-016-132387 20 0.9 1106 4 US.09-949-016-13123

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APPLICANT: Wands, Jack R.

APPLICANT: de la Monte, Suzanne M.

APPLICANT: de la Monte, Suzanne M.

APPLICANT: carlson, Rolf I.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS

FILE REFERENCE: 21466-032 DIV5

CURRENT APPLICATION NUMBER: US/09/903,248

CURRENT APPLICATION NUMBER: 09/436,184

PRIOR APPLICATION NUMBER: 09/436,184

PRIOR APPLICATION NUMBER: 09/436,184

PRIOR PLING DATE: 1999-11-08

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PALENTIN Ver. 2.1

LENGTH: 2324
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ALIGNMENTS
                                                                                  Sequence 3, Application US/09903248 Patent No. 6783758 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 2324; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CRGANISM: Homo sapiens
US-09-903-248-3
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                                                            FILING DATE: 17-MAR-1998
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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LOCATION:
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US-09-040-485-1
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A GENE ENCODING A NOVEL MARKER FOR TITLE OF INVENTION:

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NUMBER OF SEQUENCES:

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BRINKS, HOFER, GILSON & LIONE

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TOWART COWER - Suite 3600, 455 N. Cityfront

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TOWART COWER - SUITE 3600, 455 N. Cityfront

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Patent No. 6166176
GENERAL INFORMATION:
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                                                   GAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCC
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APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Garter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Retter, Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Pan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121,478C15;
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF EGO ID NOS: 1864
SOFTWARE: FastESQ for Windows Version 3.0
SEQ ID NO 1791
LENGTH: 2442
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Sequence 1791, Application US/09736457
Patent No. 6509448
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Bangur, Chaitanya S.
Lodes, Michael A.
Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
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US-09-736-457-1791
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GENERAL INFORMATION:
APPLICANT: Wang, TC
APPLICANT: Bangur,
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                      766 TCACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCA 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 GGAACTTCATTCTTCACGTGGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTA 105
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TCACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCA 941
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Pred. No. 3e-297;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                             JOHNSTON INCOMPANTATION.

APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Micheel A.
APPLICANT: Lodes, Micheel A.
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Retter, Darrick
APPLICANT: Marc
APPLICANT: Marc
APPLICANT: Marc
APPLICANT: Marnion, Jane
APPLICANT: Marnion, Jane
APPLICANT: Marc
APPLICANT: Marnion, Jane
APPLICANT: APPLICANTON: OMPOSITIONS AND METHODS FOR
ITLE OF INVERTION: OMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121, 478614
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT APPLICATION NUMBER: US/09/102,705
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1791
TENDER OF 1893
                                                                                                                                                                       RESULT 7
US-09-702-705-1791
Sequence 1791, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
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Best Local Similarity 99.9%;
Matches 690; Conservative (
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US-09-702-705-1791
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                                                                                                      522 CAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGATGAGTTTTTTTGGCGACT
                                                                                                                                                                        GATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCAT
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Patent No. 6727080

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION: GENE ENCODING LABYRINTHIN, A MARKER FOR CANCER

TITLE OF INVENTION: GENE ENCODING LABYRINTHIN, A MARKER FOR CANCER

TITLE OF INVENTION: GENE ENCODING LABYRINTHIN, A MARKER FOR CANCER

FILE REFERENCE: 21511/91057

CURRENT APPLICATION NUMBER: US/09/659,521

CURRENT FILING DATE: 1999-03-11

PRIOR APPLICATION NUMBER: 09/040,485

PRIOR APPLICATION NUMBER: 09/040,485

PRIOR FILING DATE: 1998-03-17

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.1

LENGTH: 2442
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Pred. No. 3e-297;
0; Mismatches 1; Indels
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90; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: (70
US-09-659-521-1
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Matches 690;
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US-09-659-521-1
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                                                                      GATGTAGATGATTTGAGATTTGAGACCCTGGAACTTGAAGTATCTCATGAAGAAACCGAGCAT
                                                                                                                                             TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCAT
                                                                                                                                                                                                                                                           GATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA
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                                                                                                                      AGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGATGATG
                                                                                                                                                                                          TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCAT
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Pred. No. 3e-297;
0; Mismatches , 1; Indels
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APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Forder, Gary
APPLICANT: Forder, Darrick
APPLICANT: Vedvick, Tom
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Ran, Liqun
APPLICANT: Ran, Liqun
APPLICANT: An Universion Compositions and Methods For THE
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILER REFERENCE: 210121.478C12
CURRENT APPLICATION WMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
                                                                                                                                                                                                                                                                                                                             AATGAAGGGATAGAAATCACAGAAGTAACTG 852
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; ORGANISM: Homo sapiens
US-09-671-325-1791
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US-09-671-325-1791
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SEQ ID NO 1791
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Sequence 3447, Application US/09949016

Facent No. 681239

GENERAL INFORMATION

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT FILING DATE: 2000-04-14, 755

FRIOR PELICATION NUMBER: 60/241, 755

PRIOR PLICATION NUMBER: 60/237, 768

PRIOR FILING DATE: 2000-10-20

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FasteSeQ for Windows Version 4.0

SEQ ID NO 3447

LENTH: 956
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US-09-949-106-16453, Application US/09949016

1 Sequence 16453, Application US/09949016

2 Sequence 16453, Application US/09949016

3 FACENTY OF SEQUENCE OF SEQUENC
                                         29846 GATGAGTTTCTTATGGCGACTGATGATGATGATAGATTTGAGACCCTGGAACTGAAGTA 29787
      561 GATGAGTTTCTTATGGCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTA 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          516 TIGCAACAAGAAGAIGGACCCACAGGAGAACCACAACAAGAGGAIGAITICITAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            462 TTGCAACAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGATGAGTTTCTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   576 GCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAG 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402 GCGACTGATGTAGATGATGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 956;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
4.9%; Score 115; DB 4; Length 95
Best Local Similarity 100.0%; Pred. No. 6.4e-45;
Matches 115; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                          29786 TCTCATGAAG 29777
                                                                                                                             621 TCTCATGAAG 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Human
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-00-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASISEQ for Windows Version 4.0
LENGTH: 74730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 GAGGAGCAGGTTCCTGTGGAGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAA 345
                                                                                                                                                                                                                                                          466 GATGTAGATGATAGATTTGAGACCCTGGAACTTGAAGTATCTCATGAAGAAACCGAGCAT 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATACAGATGAAGATGTAACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAA 521
                                                                                                                                                                                                                                                                                                                                          522 CAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGATGAGTTTCTTATGGCGACT 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCAT 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCAT 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.6%; Score 130; DB 4; Length 74730; Best Local Similarity 100.0%; Pred. No. 3.9e-52; Matches 130; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 AATGAAGGGATAGAAATCACAGAAGTAACTG 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            822 AATGAAGGGATAGAAATCACAGAAGTAACTG 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15189, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:
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ROGANISM: Human

FRATURE:

NAME/KEY: misc_feature

LOCATION: (1) ... (14730)

SOTHER INFORMATION: n = A,T,C or G
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Query Match
Best Local Similarity 100.0
Canage 73; Conservative
                                                                                                                                                                                                                                 322 AAGTTTTATTAGG 334
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; ORGANISM: Human
US-09-949-016-122345
US-09-949-016-122387
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; ORGANISM: Human
US-09-949-016-236
                                                                                                                                                                                                                                                                                                                                                       RESULT 16
US-09-949-016-236/c
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US-09-940-016-122387/c

i Sequence 122387, Application US/09949016

is Patent No. 6812339

i GENERAL INFORMATION:

i APPLICANT: VENTER, J. Craig et al.

i TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

if ILE REPRENCE: CL001307

i CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSOCTHARE: FaetSEQ for Windows Version 4.0

i LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICAMT: VENTER, J. Craig et al.
APPLICAMT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-041,4
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSESEE FOR WINDOWS VERSION 4.0
SEQ ID NO 122372
LENGTH: 601
                                                                    1073 GGGAAAAATTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAG 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 AGAACCCCAGAATATCGAAGATGAAGCAAAAGAAAGAAATTCAGTCCCTTCTCCCATGAAAT 209
                                                                                                    425 AGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATGAAAT 484
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.3%; Score 77; DB 4; Length 601; Best Local Similarity 100.0%; Pred. No. 1.2e-26; Matches 77; Conservative 0; Mismatches 0; Indels
                        0; Indels
  Best Local Similarity 100.0%; Pred. No. 6e-32; Matches 88; Conservative 0; Mismatches
                                                                                                                                                                 1133 TCCACGAGCAAGATATGGGAAGGCGCAG 1160
                                                                                                                                                                                                                636 recaccadecadarardecadadecedas 609
                                                                                                                                                                                                                                                                                     RESULT 14
US-09-949-016-122372/c
; Sequence 122372, Application US/09949016
; Patent No. 6812339
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ORGANISM: Human
US-09-949-016-122372
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ORGANISM: Huma
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US-09-499-016-122345/c

i Gequence 122345, Application US/09949016

patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2007012

SOFTWARE: FESTSEQ for Windows Version 4.0

SEQ ID NO 122345

LENTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 226, Application US/09949016
; Sequence 226, Application US/09949016
; Retent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VEWTER, U. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION UNMER: US/09/949,016
; CURRENT APPLICATION NUMBER: 00/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,768
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; RIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FRASESQ for Windows Version 4.0
; LEAGTH: 2208
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                                                                                                                                    TGATGTGGATGATGCCA 321
                                                                                                                                                                                           86 TAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCA 27
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                                                                  Gaps
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2.5%; Score 59; DB 4; Length 2208;
Best Local Similarity 100.0%; Pred. No. 5.2e-18;
Matches 59; Conservative 0; Mismatches 0; Indels
Length 601;
                                                                                                                                       262 TAGGAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTT
3.1%; Score 73; DB 4; Les 100.0%; Pred. No. 9.8e-25; tive 0; Mismatches 0;
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RESULT 20
US-09-859-604-10/c
is Sequence 10, Application US/09859604
is Retent No. 6835370
is GREERL INFORMATION:
is APPLICANT: Wands, Jack R.
is APPLICANT: Butch, Alan H
is APPLICANT: Ghanbari, Hossein A
if TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
if FILE REPERENCE: 21466-032 CIP
if CURRENT APPLICATION NUMBER: US/09/859,604
ic CURRENT FILING DATE: 2001-05-17
is PRIOR FILING DATE: 1999-11-08
inverse For Invention Ver. 2.1
is SEQ ID NOS: 13
invention Ver. 2.1
invention Ver. 2.1
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US-09-689-604-11/c
| US-09-689-604-11/c
| Sequence 11, Application US/09859604
| Patent No. 683370
| GENERAL INFORMATION
| APPLICANT: Wands, Jack R.
| APPLICANT: Deutch, Alan H
| APPLICANT: Glanbari, Hossein A
| TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
| TITLE REFERENCE: 21486-632 CIP
| CURRENT FILING DATE: 2001-05-17
| PRIOR PLILING DATE: 1999-11-08
| WINDER OF SEQ ID NOS: 13
| SEQ ID NO 11
| SEQ ID NO 11
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:Location (-1); OTHER INFORMATION: 0ligomucleotide
US-09-859-604-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Location (-6);
; OTHER INFORMATION: oligonucleotide
92-09-689-604-11
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Query Match 0.9%; Score 21; DB 4; Length 1845; Best Local Similarity 100.0%; Pred. No. 9.6; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.9%; Score 20; DB 4; Length 20; Best Local Similarity 100.0%; Pred. No. 29; Matches 20; Conservative 0; Mismatches 0; Indels
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0.9%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                           93 CAGCAGCGCTCCGGCAGCGG 113
                                                                                                                53 CAGCAGCGCTCCGGCAGCGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 AATGGCCCAGCGTAAGAATG 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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FREEDRING: 649307
GENERAL INFORMATION:
FREEDRING: FAILURG M. IAN
FAPPLICANT: PHILLIPS, M. IAN
FITTLE OF INVENTION: MATTERNEE COMPOSITIONS TARGETED TO BETAL-ADRENOCEPTOR-SPECIFIC mR
FITTLE OF INVENTION: MATTERNEE COMPOSITIONS TARGETED TO BETAL-ADRENOCEPTOR-SPECIFIC mR
FILE REPERENCE: 4300.01390
FILE OF INVENTION WHERE: 09/95/9/614,034
CURRENT APPLICATION NUMBER: 09/152,717
FRIOR FILING DATE: 1998-09-14
FRIOR FILING DATE: 1998-09-14
FRIOR FILING DATE: 1999-09-14
                                                                                                                                                                                                                                                             RESULT 18

19.69-494-016-13283

1 Sequence 13283, Application US/09949016

1 Patent No. 6812339

2 Geguence 13283, Application US/09949016

1 Patent No. 6812339

3 GENERAL INFORMATION

4 PEDICANT: VENYTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLO01307

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 13283

LENGTHA: 9984
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                                                                                     Gaps
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                                                                                                                                   943 CAGAAACAAATAGAAAAACAGATGATCCAGAACAAAAAGCAAAAG 987
                                                                                                                                                                 212 CAGAAACAAATAGAAAAACAGATGATGATCCAGAACAAAAAGCAAAAG 168
                                 Length 601;
                           Ouery Match 1.9%; Score 45; DB 4; Length 601
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 45; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
NAME/KEY: misc feature
LOCATION: (1828).. (1838)
COCATION: (1828).. (1838)
SHORT INFORMATION: WHERE N = A, T, C OR G
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ORGANISM: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13283
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Best Local
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APPLICANT:
APPLICANTION:
AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION:
BUEDMONIABE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE:
2709-2004001
CURRENT APPLICATION NUMBER: US,09/489,039A
CURRENT FILING DATE:
1999-01-27
PRIOR PILING DATE:
1999-01-29
NUMBER OF SEQ ID NOS:
14342
SEQ ID NO 1933
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                                                                                                    RESULT 24
US-09-489-039A-1933/c
'Sequence 1933, Application US/09489039A
'Patent No. 6610836
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                                        157 GCAACAGCAGCAGCAGCGGC 138
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43 GCAACAGCAGCAGCGGC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-489-039A-1933
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US-09-949-016-3254
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US-09-859-604-12
                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
APPLICANT: de la Monte, Suzanne M
APPLICANT: de la Monte, Suzanne M
APPLICANT: Ghanbari, Alan H
APPLICANT: Ghanbari, Hossein A
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REPERENCE: 21486-032 CIP
CURRENT APPLICATION NUMBER: US/09/859,604
CURRENT FILING DATE: 2001-05-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.9%; Score 20; DB 4; Length 20; Best Local Similarity 100.0%; Pred. No. 29; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
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OTHER INFORMATION: score 15.600003814697
OTHER INFORMATION: seq LLLLLLSPWPWMA/HV
US-09-621-976-24
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/436,184
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 20
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Patent No. 6639063
                                                                                                                                                    US-09-859-604-12/c
; Sequence 12, Application US/09859604
; Patent No. 6835370
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                        CGTGCAATGGCCCAGCGTAA 25
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                                                                20 cerecaareeccaeceraa 1
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ORGANISM: Homo sapiens
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LOCATION: 109..186
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US-09-621-976-24/c
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LENGTH: 342
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Sequence 11878, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENCRANTION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICANTON NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PRIOR FILING DATE: 2000-10-03

PRIOR PRIOR FILING DATE: 2000-10-03

PRIOR PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 11878

LENGTH A. 11668

LENGTH A. 11668
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Patent No. 6812399
GREEAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE: REFERENCE: CL001307
CURRENT APPLICATION WUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.9%; Score 20; DB 4; Length 8841; Best Local Similarity 100.0%; Pred. No. 29; Matches 20; Conservative 0; Mismatches 0; Indels
            CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION WUMBER: 60/24,755
PRIOR APPLICATION WUMBER: 60/237,768
PRIOR APPLICATION WUMBER: 60/237,768
PRIOR PRILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
LENGTH: 8841
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                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14996
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ORGANISM: Human
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US-09-949-016-13554
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| Sequence 1812, Application US/09949016
| Sequence 1812, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| TYPLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| FILE REFERENCE: CLOOJ.307
| FILE REFERENCE: 2000-10-20
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR PELLING DATE: 2000-10-20
| PRIOR PELLING DATE: 2000-10-20
| PRIOR PELLING DATE: 2000-10-20
| PRIOR PELLING DATE: 2000-00-09
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SEQ ID NO 1812
| LENGTH: 1116
| WANDER PELLING DATE: 2000-09-08
| LENGTH: PALE PELLING DATE: 2000-09-09
|
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION UNMBER: 60/2414
PRIOR PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FEALESEQ for Windows Version 4.0
SEQ ID NO 3254
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
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100.0%; Pred. No. 29;
tive 0; Mismatches 0; Indels
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0.9%; Score 20; DB 4;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches
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Patent No. 6812339
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Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3254
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ORGANISM: Human
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US-09-949-016-14996
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0.8%; Score 19;
100.0%; Pred. No.
                                                                                                       0.9%;
                                                                                                     Query Match
Best Local Similarity 100.(
Matches 20; Conservative
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US-09-513-999C-35281
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                      JS-09-949-016-15775/c
; LENCTH: 117937
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12762
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FACELL NO. POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR FILING DATE: 2000-04-14
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREEER FACELED
LENGTH: 47284
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FARENTEL NO. 1912.37

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYNORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASESEQ FOR WINGOWS VERSION 4.0
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                                                                                                                                                                                                   0.9%; Scc. 100.0%; Pred. No. 2...
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13554
LENGTH: 11713
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100.0%; Pred. No.
tive 0; Mismatch
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; Sequence 17029, Application US/09949016
; Patent No. 6812339
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                                                                                                                                                                                                                                                                                                    43 GCAACAGCAGCAGCGGC 62
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Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                               TYPE: DNA
ORGANISM: Human
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US-09-949-016-17029
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SERVERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-1,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-04

NUMBER OF SEQ ID NOS: 207012

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; Sequence 35281, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dutas Minne Edwards, J.B.
; APPLICANT: Duclett, A.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REPERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT PILING DATE: 1900-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SEQ ID NO 35281
; LENGTH: 148
                                                         Gaps
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Length 117937;
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88;
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29;
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                                                         0; Mismatches
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Sequence 4406. Application US/09248796A

Sequence 4406. Application US/09248796A

Setent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WOLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A

PRIOR FILING DATE: 1998-02-13
PRIOR PELICATION NUMBER: US 60/094,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 4406

LENGTH: 951
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US-09-49-016-1792/C

US-09-49-016-1792, Application US/09949016

Sequence 1792, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:
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88;
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(US-08-33,-214-25/c
; Sequence-25, Application US/08339214
; Patent No. 6348334
; GENERAL INFORMATION:
; APPLICANT: Nagata, Shigikazu
APPLICANT: Suda, Takashi
; APPLICANT: Takashi, Tomoniro
; APPLICANT: Nakamura, No. 634833410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1004 TAAACTTTTAAATAAATTT 1022
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; ORGANISM: Human
US-09-949-016-1792
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US-09-248-7964-13462/c
; Sequence 13462, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICAMY: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN;
; FILE REFERENCE: 107196-132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; FILE REFERENCE: 107196-132
; CURRENT PILING DATE: 1999-02-13
; PRIOR FILING DATE: 1999-02-13
; PRIOR FILING DATE: 1999-08-13
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 13462
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195-09-494-016-61822/c

195-09-494-016-61822/c

19 Sequence 61822, Application US/09949016

19 Patent No. 6812339

19 GENERAL INFORMATION: OF Craig et al.

1 TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

1 TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

2 TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

3 FRICK FILING DATE: 2000-04-14

5 FRICK FILING DATE: 2000-10-20

5 FRICK FILING DATE: 2000-10-30

6 FRICK FILING DATE: 2000-09-08

7 NUMBER OF SEQ ID NOS: 207012

7 SEQ ID NO 61822

8 SEQ ID NO 61822

8 MENTALE FABLE CATION WINDOWS VERSION 4.0

8 SEQ ID NO 61822
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   0; Mismatches
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                                                                      45 AACAGCAGCAGCAGCGGCT 63
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   Matches 19; Conservative
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CRGANISM: Human
US-09-949-016-61822
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EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER PELING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER PELING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
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EARLIER PELING DATE: 1997-05-23
                                                                                                                                                 EARLIER FILING DATE: 1997-03-0,
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,315
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/047,618
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,582
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APPLICATION NUMBER: 60/047,632
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FILING DATE: 1997-05-23
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FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,671
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APPLICATION NUMBER: 60/043,669
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APPLICATION NUMBER: 60/043,672
                                                                                   FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
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APPLICATION NUMBER: 60/047,587
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APPLICATION NUMBER: 60/047,598
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APPLICATION NUMBER: 60/047,596
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                                                     60/040,336
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APPLICATION NUMBER: 60/047,581
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APPLICATION NUMBER: 60/047,584
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APPLICATION NUMBER: 60,
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APPLICATION NUMBER: 60
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TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS: 103
CORRESPONDENCE ADDRESS: ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: P.O. Box 747
CITY: Falls Church STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,214
FILING DATE: 10-NOV-1994
FILING DATE: 10-NOV-1994
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100.0%; Pred. No. 88;
ive 0; Mismatches 0; Indels
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US-09-149-476-110/c

Sequence 110, Application US/09149476

Patent No. 6420526

GENERAL INFORMATION:
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1

CURRENT APPLICATION NUMBER: US/09/149,476

CURRENT APPLICATION NUMBER: PCT/US98/04493

EARLIER APPLICATION NUMBER: PCT/US98/04493

EARLIER FILING DATE: 1998-03-06

BARLIER FILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-03-07

EARLIER RILING DATE: 1907-03-07

EARLIER RILING DATE: 1907-03-07

EARLIER RILING DATE: 1907-03-07

EARLIER APPLICATION NUMBER: 60/040,333

EARLIER APPLICATION NUMBER: 60/040,333
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LOCATION: 74..907
OTHER INFORMATION: /label= Figs_2-3
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APPLICATION NUMBER: 60/040,626
FILING DATE: 1997-03-07
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NAME: MULPDY JI., Gerald M.
REGISTRATION UNMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110
TELECOMUNICATION INFORMATION:
TELECHONE: 703-205-8050
TELEFAX: 703-205-8050
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1623 base pairs
TYPE: nucleic acid
STRANDEDNESS: not releva
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Best Local Similarity
Matches 19; Conservi
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ORIGINAL SOURCE:
ORGANISM: rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-339-214-25
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BARLIER APPLICATION NUMBER: 60/046, 974

BARLIER FELING DATE: 1997-06-06

BARLIER APPLICATION NUMBER: 60/056, 895

BARLIER APPLICATION NUMBER: 60/056, 893

BARLIER APPLICATION NUMBER: 60/056, 893

BARLIER PILING DATE: 1997-08-22

BARLIER FILING DATE: 1997-08-22

BARLIER PAPLICATION NUMBER: 60/056, 893

BARLIER PAPLICATION NUMBER: 60/056, 910

BARLIER PAPLICATION NUMBER: 60/056, 910

BARLIER APPLICATION NUMBER: 60/056, 910

BARLIER APPLICATION NUMBER: 60/056, 910

BARLIER APPLICATION NUMBER: 60/056, 910

BARLIER PILING DATE: 1997-08-22

BARLIER PILING DATE: 1997-08-23

BARLIER PILING DATE

EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-06-23
EARLIER FILING DATE: 1997-06-23
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-06-23
EARLIER FILING DATE: 1997-

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Gaps

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0.8%; Score 19; DB 4; Length 1821; ilarity 100.0%; Pred. No. 88; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 19; Conserv

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APPLICATION NUMBER: 60/040,336
FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
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APPLICATION WUMBER: 60/047,597
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,502
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APPLICATION NUMBER: 60/047,633
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,587
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APPLICATION NUMBER: 60/047,598
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APPLICATION NUMBER: 60/047,613
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APPLICATION NUMBER: 60/043,580
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APPLICATION NUMBER: 60/043,568
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APPLICATION NUMBER: 60/043,569
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APPLICATION NUMBER: 60/043,312
60/038,621
                                                                 FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,334
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APPLICATION NUMBER: 60/047,592
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APPLICATION NUMBER: 60/047,584
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                                                                                                              FILING DATE: 1997-03-07
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APPLICATION NUMBER:
                                          APPLICATION NUMBER:
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Pred. No. 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION: 186 Human Secreted proteins TITLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: P2002P1
FURBAY APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
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100.0%; Pred. No. co...
0; Mismatches
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; Sequence 49, Application US/09620312D
; Patent No. 6569662
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Patent No. 6420526
GENERAL INFORMATION:
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                                                                 437 AGCAGCGCCACACACACACA 455
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SEQ ID NO 49
LENGTH: 2286
                        36 AGCAGCGGCAACAGCAGCA 54
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Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Best Local Similarity 100.(
Matches 19; Conservative
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Zhao, Qing A.
Wehrman, Tom
                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
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Wang, Jian-Rui
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Xue, Aidong
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ORGANISM: Homo sapiens
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; LOCATION: (69)..(1727)
US-09-620-312D-49
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EARLIER PILING DATE: 1997-04-11
EARLIER PLING DATE: 1997-06-06
EARLIER PLING DATE: 1997-06-06
EARLIER PLING DATE: 1997-06-05
EARLIER PLING DATE: 1997-06-20
EARLIER APPLICATION NUMBER: 60/056,693
EARLIER APPLICATION NUMBER: 60/056,693
EARLIER APPLICATION NUMBER: 60/056,693
EARLIER PLING DATE: 1997-06-20
EARLIE
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RESULT 44

US-09-949-016-2642

i Sequence 2642, Application US/09949016

patent No. 6812339

i GENERAL INFORMATION:
TITLE OF INVENTION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PILE REPRENCE: CLO01307

CURRENT PAPLICATION NUMBER: US/09/949,016

CURRENT PAPLICATION NUMBER: 60/241,755

PRIOR PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR PRIOR PAPLICATION NUMBER: 60/231,498

PRIOR PRIOR TILING DATE: 2000-10-03

PRIOR PRIOR PRIOR TO NUMBER: 60/231,498

PRIOR PRIOR PRIOR TO NUMBER: 60/231,498

PRIOR PRIOR PRIOR TO NUMBER: 60/231,498

SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 207012

TYPE: NNA

TYPE: DNA ORGANISM: Human

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Gaps

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Sequence 14384, Application US/09949016

Sequence 14384, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASSECE for Windows Version 4.0

SEQ ID NO 14384
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General Information US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AL.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AL.

FILE REFERENCE: CLO01307.

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

SOFTWARE PERSON OF SEQ ID NOS: 207012

SOFTWARE PERSON OF SEQ ID NOS: 207012

SEQ ID NO 12375

LENGTH: 7460
          10.8%; Score 19; DB 4; Length 6625; Darity 100.0%; Pred. No. 87; Conservative 0; Mismatches 0; Indels
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                                                        0; Mismatches
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Best Local Similarity
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                                     Best Local Similarity
Matches 19; Conserv
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Best Local Similarity
Matches 19; Conserv
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                      Query Match
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Sequence 633, Application US/09949016

Patent No. 6812339

HINTER NO. 6812339

TITLE OF INVENTION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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                                     Score 19; DB 4;
Pred. No. 88;
                        0.8%; Scor.
100.0%; Pred. No. cc.
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SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 633
LENGTH: 3482
                                                                                                                    1777 CTTTAGAAAGAAACTGGAA 1795
                                                                                                                                                            2966 CTTTAGAAAGAACTGGAA 2984
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LOCATION: (1)...(3482)
CTHER INFORMATION: n = A,T,C or G
US-09-949-016-633
                                                                            Conservative
                    Query Match
Best Local Similarity
...-hes 19; Conserve
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US-09-949-016-2642
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RESULT 51

US-09-949-016-11868/C

Sequence 11866, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
TILLE OF INVENTION:
TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILLE OF INVENTION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 11868

LENGTHALS TABLESEQ FOR WINDOWS VERSION 4.0

LENGTHALS TABLESEQ FOR WINDOWS VERSION 4.0
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86;
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18759 AGCAGCGCCAACAGCAGCA 18777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
; LOCATION: (1) ... (300598)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11868
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; LOCATION: (1)...(302604)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14588
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ORGANISM: Human
FEATURE:
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ORGANISM: Human
FEATURE:
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                                                                                                              Sequence 15619, Application US/09949016

Facent No. 681239

GENERAL INFORMATION:

APPLICANT: WENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PELING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

SOFTWARE FEESE FEESEQ for Windows Version 4.0

LENGTH: 7700

LENGTH: 7700
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    1777 CTTTAGAAAGAAACTGGAA 1795
                             4966 CTTTAGAAGAAACTGGAA 4984
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) LOCATION: (1)...(28843)

) OTHER INFORMATION: n = A,T,C or G

US-09-949-016-17325
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ORGANISM: Human
                                                                                          RESULT 49
US-09-949-016-15619
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; ORGANISM: Human
US-09-949-016-15619
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36 AGCAGCGGCAACAGCAGCA 54

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TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENTER.

APPLICANT: VENTER.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DIGEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DIGEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASEESEQ FOR WINDOWS Version 4.0

LENGTH: 302604
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FACELL NO. 9812313
FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
FRICK APPLICATION NUMBER: 60/241,755
FRICK FILING DATE: 2000-04-14
FRICK FILING DATE: 2000-10-20
FRICK PRICK APPLICATION NUMBER: 60/231,768
FRICK FILING DATE: 2000-10-03
FRICK FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASESEQ FOR WINDOWS Version 4.0
SEQ ID NO 17119
FRICK FILING DATE: 2000-09-08
FRICK FILING DATE: 2001-09-08
FRICK FILIN
Gaps
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    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.8%; Score 19; DB
100.0%; Pred. No. 86;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               . Sequence 14589, Application US/09949016 ; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-949-016-17119/c
; Sequence 17119, Application US/09949016
; Patent No. 6812339
                                                                                                                                                            299448 GGGGAAAATTGAGGAAGC 299430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299448 GGGGAAAATTGAGGAAGC 299430
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                                                                                    1072 GGGGAAAATTGAGGAAGC 1090
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| LOCATION: (1)...(302664)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
| LOCATION: (1) ... (308362)
| OTHER INFORMATION: n = A,T,C
US-09-949-016-17119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
    Matches 19; Conservative
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Matches 19; Conserv
                                                                                                                                                                                                                                                                                       RESULT 53
US-09-949-016-14589/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Sequence 12777/C

| Sequence 12777, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WIMBER: US/09/949,016
| CURRENT APPLICATION WIMBER: 06/241,755
| PRIOR FILING DATE: 2000-04-14
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
| WUMBER OF SEQ ID NOS: 207012
| SOFTWARE: PEASLED for Windows Version 4.0
| SEQ ID NO 12777
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APPLICANT: Wands, Jack R.

APPLICANT: Wands, Jack R.

APPLICANT: Genetch, Alan H

APPLICANT:
                                                                                                     Gaps
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     Length 308362;
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US-09-859-604-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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DB 4;
86;
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Query Match

0.8%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 86;
Matches 19; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                  299264 GGGGAAAATTGAGGAAGC 299246
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                                                                                                                                                                                                 1072 GGGGAAAATTGAGGAAGC 1090
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; LOCATION: (1)...(828152)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12777
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MS-09-513-999C-10601

### Sequence 10601 Application US/09513999C

### SPEIGNAT Durak Milne Edwards, J.B.

### APPLICANT: Durak Milne Edwards, J.B.

### APPLICANT: Durak Milne Edwards, J.B.

### APPLICANT: Durak Milne Edwards, J.B.

### PRICA PRIVENTION: Expressed Sequence Tags and Encoded Human Proteins.

### PRIVENT REPRENCE: 59.US2.44

### PRIOR PEPLICATION NUMBER: US 60/122,487

### PEPLIC
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10S-02-270-767-10408
1 Sequence 10408, Application US/09270767
2 Patent No. 6703491
2 GENERAL INFORMATION:
3 APPLICANT: Homburger et al.
3 TILE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; FILE REFERENCE: File Reference: 7326-094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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CLASSIFICATION: 514

PRIOR APPLICATION DATA
APPLICATION NUMBER: FR 94-07191
FILING DATE: 13-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 017753-058
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGHH: 319 Base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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1 LOCATION: 440

US-09-513-999C-10601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-482-842B-2
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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APPLICANT: CHASKIN, Daminique
APPLICANT: CHASKIN, Dominique
APPLICANT: CHASKIN, Dominique
APPLICANT: BELLET, Dominique
APPLICANT: BELLET, Dominique
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF THIS PROTEIN AND
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF THIS PROTEIN AND
TITLE OF INVENTION: SAID PROTEIN
TITLE OF INVENTION: SAID PROTEIN
ADDRESSEE: BUTNS, Doane, Swecker & Mathis
STREET: P. O. Box 1404
CORRESPONDENCE ADDRESS:
ADDRESSEE: Butns, Doane, Swecker & Mathis
STREET: P. O. Box 1404
CITY: Alexandria
STREET: P. O. Box 1404
COUNTRY: United States
INP Compatible FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: DatentIn Release #1.0, Version #1.30
CURPUTER: DATENTIN BALES FORM:
MEDIUM TYPE: US/08/482.842B
FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US
CURRENT PEPLICAND NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SEQ ID NO 3024
LENGTH: 286
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                                                  Ouery Match 0.8%; Score 18; DB 4; Length 22; Best Local Similarity 1000%; Pred. No. 2.7%+0.2; Matches 18; Conservative 0; Mismatches 0; Indels
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GRGANISM: Zea mays

FRATURE:
NAME/KEY: misc_feature

NAME/KEY: unsure

LOCATION: 87, 108, 146, 200, 239

OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.8%; Score 18; DB 4; L. Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3024, Application US/09313294A Patent No. 6476212 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-482-842B-2
; Sequence 2. Application US/08482842B
Patent No. 5910480
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 CAACAGCAGCAGCAG 198
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                                                                                                                                                                                    8 TGCAATGGCCCAGCGTAA 25
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US-09-313-294A-3024
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Sequence 36982 Application US/09949016

Patent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFREENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastesQ for Windows Version 4.0

SEQ ID NO 36982
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Sequence 40425, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
PATENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERBENCE: CLOOKINSOT
CURRENT APPLICATION NUMBER: US/99/949,016

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 40425

LENGTH: 601
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                              2100 AAGGAAGGCTGCAAGATT 2117
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                                                                                  349 AAGGAAGGCTGCAAGATT 332
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US-09-949-016-40425
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100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                      Length 529;
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET. 054PR2
CURRENT FILIAGO DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16896
LENGTH: 561
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0.8%; Score 18; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0;
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0.8%; Score 18; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0;
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US-09-918-686-4/c

Sequence 4, Application US/09918686

Patent No. 6475739

GENERAL INFORMATION:

APPLICANT: Brunkow, Mary

APPLICANT: Paeper, Bryan

APPLICANT: Reachling-Hampton, Karen

TITLE OF INVENTION: GENOMIC DELETIONS

WINDER APPLICATION NUMBER: US/09/918,686

CURRENT FILING DATE: 2001-07-30

NUMBER OF SEQ ID NOS: 105

SEQ ID NO 4

LENGTH: SS7

TRUE THE SS7
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SEQ ID NO 10408
LENGTH: 529
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; Patent No. 6639063
                                                                                                                                             ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10408
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Matches 18; Conservative
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Sequence 42138, Application US/09949016

| Sequence 42138, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION
| TILLS OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| CURRENT FILLING DATE: 2000-00-414
| FRIOR PRILING DATE: 2000-00-20
| PRIOR FILLING DATE: 2000-10-20
| PRIOR FILLING DATE: 2000-10-30
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: 02/02/04-14
PRIOR PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-3
PRIOR PILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-09
RIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 42137
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US-09-349-016-42139
US-09-349-016-42139, Application US/09949016
| Patent No. 6812339 |
| GENERAL INFORMATION: |
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| FILE REPERENCE: CL001307
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100.0%; Pred. No. 2.7e+02;
0; Indels
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; ORGANISM: Human
US-09-949-016-42137
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US-09-949-016-42138
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; ORGANISM: Human
US-09-949-016-42138
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| Sequence 42136, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: URNTER, US.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| FILE REPRENCE: CLO01307 |
| CURRENT FILING DATE: 2000-04-14 |
| PRIOR FILING DATE: 2000-04-14 |
| PRIOR FILING DATE: 2000-10-20 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SEQ ID NO 42136 |
| LENTH: 601
                                             GENERAL INFORMATION:

GENERAL INFORMATION:

FACE OF 1949-016-42135

GENERAL INFORMATION:

FACE OF INVENTION:

FALL OF INVENTION:

TITLE OF INVENTION:

FILE OF INVENTI
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US-09-949-016-42137
Sequence 42137, Application US/09949016
; Patent No. 6812339
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; ORGANISM: Human
US-09-949-016-42135
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US-09-949-016-42136
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US-09-949-016-42136
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-53139
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US-09-949-016-67303
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Sequence 42140, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERRICE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: FBSESEQ for Windows Version 4.0

SEQ ID NO 42140
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US-09-944-016-53139/c

1 US-09-944-016-53139, Application US/09949016

1 Sequence 5313.9, Application US/09949016

2 Sequence 5313.9, Application US/09949016

3 GENERAL INFORMATION:

4 APPLICANT:

5 TITLE OF INVENTION:

7 TITLE OF INVENTION:

8 TITLE OF INVENTION:

7 TITLE OF INVENTION:

8 TITLE OF INVENTION:

8 TITLE OF INVENTION:

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live 0; Mismatches 0; Indels
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0.8%; Score 18; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0;
                               CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 42139
CURRENT APPLICATION NUMBER: US/09/949,016
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Matches 18; Conserva
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; ORGANISM: Human
US-09-949-016-42139
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US-09-949-016-42140
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SERVERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTON: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTON: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTON: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-10-10

PRIOR FILING DATE: 2000-10-03

WUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASESEQ FOR Windows Version 4.0

SEQ ID NO 67303
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Sequence 69417, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PPLICATION NUMBER: 60/241,755

PRIOR PPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-0-06

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASESEQ for Windows Version 4.0
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100.0%; Pred. No. 2.7e+02;
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Best Local Similarity 100.0%; Pred. No. 2.7

Matches 18; Conservative 0; Mismatches
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 53139
LENGTH: 601
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; Patent No. 6812339
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US-09-449-016-69418/C

US-09-449-016-69418/C

Sequence 69419, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION NUMBER: 08/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 69418

LENGTH: EMSCRED
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Sequence 64419, Application US/09949016

Fatent No. 6812339

GENERAL INFORMATION

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: DATE: 2000-04-14

FILE REFERENCE: LOO1307

CURRENT FILING DATE: 2000-04-14

FRIOR PRILING DATE: 2000-10-20

FRIOR PELICATION NUMBER: 60/237,768

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FasteEQ for Windows Version 4.0

SEQ ID NO 69419

LENGTH: 601

TYPE: DAM A
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US-09-949-016-69419/c
; SEQ ID NO 69417
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-69417
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; ORGANISM: Human
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Query Match 0.8%; Score 18; DB 4; Length 601
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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Search completed: March 25, 2005, 22:35:18 Job time : 417 secs

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